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100.0%; Score 564; DB 6; Length 564; 100.0%; Pred. No. 4e-171; tive 0; Mismatches 0; Indels (
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JP 2001516225-A/1.
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Best Local Similarity 100.
Matches 564; Conservative
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ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
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M83827 Orgyia pseu

U7930 Orgyia pseu

S64501 ps.9=8.9 kd

AX766573 Sequence

AY043265 Epiphyas

AY445471 Rachiplus
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L22858 Autographa
AY327402 Choriston
BD187790 A virus i
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AF512031 Choriston
D14467 Bombyx mori
M59422 Autographa
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AF246708 Spodopter
AF325155 Spodopter
                                                        October 24, 2005, 18:40:53 ; Search time 3416.8 Seconds (without alignments) 7998.346 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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4 AY043265

4 AY145471

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NPHRENIEN
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Maximum Match 100%
Listing first 45 summaries
                                      - nucleic search, using sw model
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99b ro: *
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Maximum DB
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U67264 Helicoverpa
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AP006270 Adoxophye
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AX767469 Sequence
CR376837 Danio rer
BX000999 Zebrafish
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AX167545 Sequence
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AC4003184 Drosophil
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            AF107100 Ecotropis
AY126275 Mamestra
AF303045 Helicover
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AC123846 Mus muscu
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Grigliatti, T.A., Theilmann, D.A., Pfeifer, T.A. and Hegedus, D.D.
Insect expression vectors
Insect expression vectors
Insect expression vectors

AL Patent: JP 2001516225-4 1 25-SEP-2001;
THE UNIVERSITY OF BRITTSH COLUMBIA
OS Multicapsid nucleopolyhedrovirus
PD 25-SEP-2001
PD 25-SEP-2001
PP 26-MAR-1999 JP 1998541010
PR 27-MAR-1997 US 60/049946,28-JAN-1998 CA 2221819 PI
THOMAS A GRIGILATTI, DAVE A THEILMANN, THOWAS
A PFEIFER, DWAYNE D
PI HGGEDUS
C C 12N15/85,C12N5/06,C12N15/69/C12N9/22
CC Insect expression vectors
FH Key
Location/Qualifiers
FT Source
Location/Qualifiers
FT FT Lorder
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                     TTTTCATGTTTGCCAACAAGCACCTTTATATACTCGGTGGCCTCCCCACCACCAACTTTTTT
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Orgyja pseudotsugata single capsid nuclopolyhedrovirus

Orgyja pseudotsugata single capsid nuclopolyhedrovirus

Orgyja pseudotsugata single capsid nuclopolyhedrovirus

Viruses; dsDNA viruses, no RNA stage; Baculoviridae;

Nucleopolyhedrovirus.

1 (bases 1 to 4170)

Theilmann,DAA and Stewart,S.

Molecular analysis of the trans-activating IE-2 gene of Orgyja pseudotsugata multicapsid nuclear polyhedrosis virus
                                                                                                                                                  GTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACACTACCACAC
                                                                                                                                                                                                                              GACAGGACGCCAGCTTCCTGTGTTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
                                                                          trans-activator (IE-2) gene, complete cds; ORF, complete cds
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| MRRRQQYNDPAALKNVRNLMARDFVFCLTRFNPECRSTDYKQIAKHSFLASRHDYI" 946. ,2370 | 3 24 | / dd. XTET="-"1 1294919" / tanslation="MMERQYQSVRSYLINNQHNAIAAGPFLQRVAGPEAHSVGRNVGD / translation="MMERGYQSVRSYLINNQHNAIAAGPFLQRVAGPEAHSVGRNVGD RAVRLARQAVLDLLKLABDIAAYMQADQPEASSRHFATLNRMRLLLIGVQDPDAR RNLNSVLARIEALLRVDVNDAEVNVLSGDFYEEXQRTFATPATPFATPFAAGOTO RNLNSVLARIEALMAAGONVLSGDFYEEXGENTERSASQQTQ | ISLEKKUJSKALIJARALYOUTFINOSEKSIVAINALKUJIUETAILENIJUETAILENIJUETAILENIJUETAILENIJUETAILENIJUETAILENIJUETAILENIJUETAILENIJUETAILENIJUETAILENIJUETAILENIJUETAILENIJUETAILENIJUETAILENIJUETAILENINA UYTSMEPEPEPERAUDITTSMEPEPEMOUDAISMEPEPEPEPEPEPEPEPENINA INNILIDAMVAETINKNAGDIRESALDOIKQGKTLKKTQPADGAPATDERSTLLSEIRQ GKTRKKIRK ERKERTENIJUETAILENITUETAILENIJUURUUTAILUETAILUURUURUURUURUURUURUURUURUURUURUURUURUUR | AKAFAKHILONSJOWKUD" complement (253) .3370) /note="ORP3; ph; similar to AcMNPV ORF8" /codon_start=1 | /product="polyheerin" /protein_id="AAC39002_1" /db_xref="G1:1911249" /translat.ton="MPPYSYRETIGRTYVYDNKYYKNLGSVIKNAKRKKHILEHEEDE kHindinHwwwafaperigerigerynki'filfrefidhykphymki'iVwwGKFFIRFWRFF | VEDS PINNOBEWNDVERTOWNRPTRPNRCYKFLAQHALRWCDVVPHEVIRIVEPSY VGMNNEYRRSPRYKCYKFLAQHALRWCDVVPHEVIRIVEPSY VGMNNEYRRSPRYKCYKFLAQHALRWCDVVPHEVIRIVEPSY VGMNNEYRRSPRYKVEFRAPDAPLIFTGPAY" EILIEVSLVFKVKEFRAPDAPLIFTGPAY" COMDJement (3350, 3354) | /note="ORF4" /codom_statr=== /rordingt==interem" | /procein_id="AAC59003.1" /procein_id="AAC59003.1" /db.xrefe="[1.1911250" /db.xrefe="1.1911250" /db.xrefe="1.1911250" | / ranstarion="mixinncacyrentilynnxhkucuscymcubursmurh MFEHWFCCLRIYVQQKIKH" complement (3698 4093) | /note="ORF5" /codon start=1 | /product="unknown" /protein_id="AAC59004.1" /db xref="G1:191151" | /translation="MGASQNSEQKILKLFYRWSSQTGAALDDEKDLHCLYDLERFVGA HLNRKADDKKRKKKCAEKAALKRVETAADRHMLEAAAAPACADDGRWSTLSRAQLDDI APEKETIVNETHDIOLKURGILKKNETAREN | complement (4125. 4719) /note="ORF6; lef-2; similar to ACMNPV ORF6" | /codon_start=1 /product==languagession factor 2" | /procent id="AACSSOS.1" Ab_xref="[4] 111252" /*=n=1=1fon="WRWWINDAAGIDG!.KRSRTVI.VDPHDFVGVI.TI.SPYTVFRRGI.F | VRMSGARLLALIZAAPKPOEPOPAVRRFPORSRRNVCLKACADGAOSLAKVLAARVSMP PCMSKTWADLSSAPRGNMYRKRFEFNCYLANVITCTKCKTACLIGALLHFYRMDAKCV | GEVTHLLIKAQDVXKPSNCAKMKKVTKLCPQASMCKGLNPICNF" complement (4742 4975) | /note=.ukr.; similar to Acmurv Okrs /codon_start=1 /broduct="unknown" | /protein id="AAC59006.1" /db_xref="GI:1911253" | <pre>/translation="MNRPTMRNTAAVTTDYDREQLRREINSLRRSVHELCTRSATGFD</pre> | >>vcv | /product="unknown" /protein_id="AAC59007.1" | /db_xrei="dl:1911254" /translatio="mgarFyRFSLRLTQEFKENVVAHVDHLMGLRALIDGKVTSADV precei.spantivsa-makuvnvovyapnatinkeHOptTYFRVCNCHAMADVPADDHS | <pre>IARYLLAECGAVLVIDHPLDVFGETEEGVNELLEVQRINAGGDL" complement (56696151) /note="ORF9; ptp-2"</pre> | |
|---|---|--|---|--|---|---|--|--|---|--------------------------------|--|---|--|--|---|---|---|---|--|---|--|--|--|---|--|
| CDS | | | | CDS | | SCO | | | CDS | | | | CDS | | | | CDS | | | | SA | | | CDS | |
| 490 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 549 | 421 GGACGCGCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC 480 | 481 GTCCCGCTTATCGCCCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG 540 | 541 CATCHGTTACAGCGACACATG 564 | OPU75930 131995 bp, DNA circular VRI | N Orgyla pseudotsugata genome. U75930 U75930.2 GI:1102498 | Org Organ | | | virology 229 97271300 9126251 | | | | | | | Chemistry, Corvallis, OR 9731-7301, USA Sequence update by submitter | | Φ | /wol_type="genomic DNA" /db_xref="taxon:164623" | /note="similar to Autographa californica nuclear polyhedrosis virus (AcMNPV) deposited in GenBank Accession | Number 122858" complement (123947) /note="ORF1; bk-1; similar to AcMNPV ORF10" | /codon_start=1 /product="protein kinase 1" | /protein id="AAC59000.1" / db xref="G1:91147" / reardlefion-whom an occopy and a driving degraming by the process of the second of the secon | KKTTAMATESADET INVHDIMSDHPSFYDNYFCYSSPTAMA I WMDYVPCPDI.FETLQTQ GALDNALVVNI VRQLCDALNDLHNATGY I HNDVKLENVI Y FGARDRVY LCDYGLCKRE HSPVHDGTLEY FSPEKI RRHNYARS FDWYANGVLAYKLL I TGGRHPFERSADEVLDLAS | |
| qa | oy ob | oy Op | Qy Dp | RESULT 3 OPU75930 LOCUS | ACCESSION VERSION KEYWORDS | SOURCE | REFERENCE AUTHORS | TITLE | MEDLINE PUBMED | REFERENCE AUTHORS | TITLE | REFERENCE AUTHORS | JOURNAL | REFERENCE | TITLE | REMARK | COMMENT FEATURES | sourc | | | CDS | | | | |

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128652 GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAAAAACACAGTTGAACAG
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Genomic, 1429 nt].
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1 (bases 1 to 1429)

Wu,X., Stewart,S. and Theilmann,D.A.

Mu,X., Stewart,S. and Theilmann,D.A.

porterin from the Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus

Olymedrosis virus

J, Gen. Virol. 74 (Pt 8), 1591-1598 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                     128232 TTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTGGCCTCCCCACCACCAACTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128472 GGGTCGCGTCCTGTACGAATCACATTATCGGACCGGACGAGTGTTGTTTATCGT
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                                                                                                                                                                                                                                                   128172 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACTATCTGTTGAAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA
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                                                                                                                                                                                                                                                                                                                                                                               TITICATGITIGCCAACAAGCACCTITIATACTCGGTGGCCTCCCCACCACCAACTTTTTT
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/organism="Orgyia pseudotsugata multicapsid
nucleopolyhadrovirus"
/mol_type="genomic DNA"
/db_xref="taxon:164623"
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p8.9=8.9 kda basic protein [Orgyia
nuclear polyhedrosis virus OpMNPV,
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/ Codon start="1"
/ product="unknown"
/ produ
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/note="ORF13; lef-1; similar to AcMNPV ORF14"
/codoin_start=1
/product="late expression factor 1"
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11547. .12140
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9893. .11362
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100.0%; Pred. No. 8.6e-166;
tive 0; Mismatches 0; Indels
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                                                                                                                       561. .566
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                                                                                                                                                                                                                                                                                                                                                                                             note="Ncol site"
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2294. .2299
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/note="BamHI
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/note="ClaI s
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                                                                                                       /proteIn_id="AAB27738.1"
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                                                                                                                                                                                                    99.7%; Score 562.4; DB 14; Length 1429; 99.8%; Pred. No. 1.6e-170; ive 0; Mismatches 1; Indels 0;
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763. .990
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/note="8.9 kda basic protein"
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Sequence 60 from Patent WO03042244.
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ACCESSION
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KEYWORDS
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TITLE
JOURNAL
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GEVTHLLIKSQDVYRENCKAKSMKLCPQANMCKGLNPICNF"
complement (2717. .3070)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MIYLRYYIFFVPFRESRTKSKKRRISHIKLFLFYATLHYNMNRR
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complement (2104. .2715)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MADARFLRFSTRLTEEYKENVVAQIDHLTNLRALINAKTTIANV
REFSEVDRAMEVAACMOVITHTYASSDDKITLOPEQLYFRVCRFCNELADVPDPDHS
ITRYLCAACGGTCLVNDPLNVFTEDGVQRFMEIQRINAGGEP"
complement (3426. .3935)
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/note="ORF9; unique to EppoMNPV"
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complement(3426. .3935)
.2090)
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product="unknown"
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                                                                                                                                                                                                                                                     /gene="lef-2'
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/note="ORF6"
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/note="ORF8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="ORF5"
                          note="ORF3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPPLTPHQVPPPPPPPPTTPLQGLLPVRDVEATPSPPSTLSKSTTLDEFEYFSNASMIQ
PPVPPTREIL PVRPHIKEKTII ISBLPDMPATNNIDDQGLAPAPPPPPPPPPPPP
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IKKGVTLKPSKTNKSDKKVDDRADLANSI KIGVKLKPIKVNTNQPLPBAPVTDISVIA
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                                                                                                                                                                                                AY043265 118584 bp DNA circular VRL 19-AUG-2001
Epiphyas postvittana nucleopolyhedrovirus, complete genome.
AY043265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MDRQYQSVKSYLIKNANNAFDANAFLTLIAGPEAHNVKQNLIGG
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LANIVSRVEHLLRYEIVNDVEITTLSGDFYEEYSKYAARQYALSIQMPPPPPVITPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTLKKRRANISQSESSSESNSSQSWDEBGNTQTIRKANKDHLKYAVNLYNFFATTHAY
RTNSELPKLLDNVFSLLDRKPRSVENVNEAKNILDNLKERVKLTSNQLDNAEAQSLYI
NDPNQFYIQVEDLIFAGRYADAKMHLDLAITESGNDERLRRLKKFANDLDAVVV"
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and Ward,V.K.
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Submitted (03-JUL-2001) Microbiology, University of Otago,
                                                                                                                                                                                                                                                                                                                                            Epiphyas postvittana nucleopolyhedrovirus
Viruses, dsDNA viruses, no RNA stage, Baculoviridae,
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete sequence of the Epiphyas postvittana
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1. .118584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleopolyhedrovirus genome
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                                                                                                                                                                                                                                                                          AY043265.1 GI:15213125
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                                                                       CATCTGTT 552
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14732 CTACGAATCGTAGACTATTTAACTTGAATAGTCTACACTGTTCTATACGCTCCTAATACA 114673
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VKEFTEKCPGMLVGVHCTHGINRTGYMVCRYLMHTLGIAPQEAIDRFEKARGHKIERQ
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                                                                                                                                                                                                          circular VRL 07-JUL-2003
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Bonning, B.C. and Harrison, R.L.
Direct Submission
Submitted (28-AUG-2002) Entomology, Iowa State University, Ames,
                                                                                                                                                                                                          AY145471 131526 bp DNA circular VRL 07-JUI
Rachiplusia ou multiple nucleopolyhedrovirus, complete genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
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join[131515. .131526,1. .326)
/note="consists of 30 bp imperfect palindromes; hrl;
replication origin"
                                                                                                                                                                                                                                                                                                                                                                                          Nucleopolyhedrovirus.

1 (bases 248 to 8029)

Harrison.R.L. and Bonning, B.C.

The nucleopolyhedroviruses of Rachiplusia ou and Anagrapha faldifera are isolates of the same virus

J. Gen. Virol. 80 (Pt 10), 2793-2798 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harrison, R. L. and Bonning, B. C.
Comparative analysis of the genomes of Rachiplusia ou and Autographa californica multiple nucleopolyhedroviruses J. Gen. Virol. 84 (Pt 7), 1827-1842 (2003)
                                                                          Rachiplusia ou multiple nucleopolyhedrovirus
Rachiplusia ou multiple nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                CTACCACACTTGAACCTTTTTGCAGTGCAAAAAAGTACGTGT
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product="unknown"
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AY145471.1 GI:23476465
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/db xrefe = dg: 12213137"

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LLKIOPGSPTPTPIRELNNNVQLLLLALHPVYDNNRPVPBSVQYLGGGLHLTQTQPQNI

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                                                                                                                                                                                                                                KTVLKHIKTLNVNSDKFINAHKLFENQVCARFEQLEQRLETLERVPDAPTMPGVIFPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="AAK85577.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQVI AQLRKTRLSFTKLTQLQKKRVRNMQRLVRKKNNI IADLAAQLERRRCRSKGSK
FAVI CQNGVLITISGSGQFVRQRVANMCAVGGEQI FCERRNDCARDRQLIAEALAAS
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                                                                                                                                                          /translation="MFDWMFGWWSFNEOHQOHHPLANHFNAQDYKOYAVDRRAQSDLVNNRSVPKCHPFTFKFRYVIDDDNGRCCRVVDFCKGLEINHELMLNCKWDSKHVRHLNBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MDLTITLIPISLKNIEEPKRSECFKLTSMREDAEFCLNVKCRSP
                                                                                                                                                                                                          VFKTPPVEISPDSMGTVYATKHGLIQILQQLSFEYKDDVLLAIKTDKGYDCDDVRDNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.8%; Score 111.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein_id="AAK85578.1"
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                                                                                                            /protein_id="AAK85574.1"
/db_xref="GI:15213135"
                                                                                                                                                                                                                                                                                                      complement (6427. .7182)
                                                                                                                                                                                                                                                                                                                         /gene="lef-1"
complement (6427. .7182)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon start=1
                                                                     'codon_start=1
'product="unknown"
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                        complement (5531.
/note="ORF10"
                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="LEF-1"
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codon_start=1
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/note="ORF13"
                                                                                                                                                                                                                                                                                                                                                                       gene="lef-1"
                                                                                                                                                                                                                                                                                                                                                                                             note="ORF11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1497. .10123
'note="ORF14"
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/gene="egt"
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/gene="egt"
7254. .8732
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Conservative
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Matches
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/translation="MYVCYTYLAALMMKRRHCKLNSLPQELFEKIVEYLSLSDYCNLVCKRPSKYNVIFDSINHQHLKGVYKKTDVQITNYNKYINCICNELRQDEFYAKSS VALSIGGGAATIFSVTNKOVEMKYHLXNVALVESEDCNEFYPFEPTSDCLICKQKNQ CPRNSF IVSLCKYMKKOVVOSNFIYYLYEINT"
complement (8253. .9239)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (9128. .9931)
/note="lef-1; rol2; ac14-like"
/note="lef-1; rol2; ac14-like"
/codon start=1
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/product="late expression factor - 1"
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PAHCVREAVRLYVPHIQESNFDALTLGYWPDVDRDIFCNVNKQIRAFYSKYFSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIVFHKPSSKRDLNSLGALFATKHGLLEILMQLNFANKSNALLHIQTEGERDDLRDKI
ESVLKHVKKLNANSEKFMVTHETFKNEVGNRFEQFELRLHELDAKLNMLQSAEKLKTA
VVTESQNGTVTFPRDITKHQHLAVFSERIDDRIKLAFVLGQERHFRKRKMRFEDDMEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /trānslation="MT1LCWLALLSTLTAVNAANILAVFPTPAYSHHIVYKVYIEALA
EKCHNVTVVKPKLFEYSTKTYCGNITEINADMSVQQYKKLVANSAMFRKRGVVSDTDT
VTAANYLGLIEMFKDQFDNINVRNFIANNQTFDLVVVEAFADYALVFGHLYDPAPVIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IAPCYGLAENFDTVGAVARHPVYHPNIWRNNFDDTEANVWTEMRLYKEFKILANMSNA
LLKQQFGPNTPTIEKLRNKVQLLLINLHPIFDNNRPVPPSVQYLGGGIHLVKNAPSTK
LNPVINAQMNKSKSGTIYVSFGSSIDTKSFANEFLYMLINTFKTLDDYTILWKIDDEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MLSWLWNWWWMWSSDNDSDDVIAVEDRFNPDDYKKYHINAQQWSH
IVKWDSFKCNTHTFKYRYVHSDTNAKCYNVIDFCKGLEIAHDDILDCNWDGDQIYHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKNITLPVIVITQNWFNORAVLGHKKMVAFITQGGLOSSDBALEAQIPMICLPNMGDQ
FYHAHKLQQLGVARALDTVTVSSDQLTVAINDMLFNAPIYKKHMAELYALINHDKATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MLFIIYLVFLRGALCGCALSAFINAHQPKQVIIVPGRSKAKHQ"
DFGRQCKDVYKNLKDVFDVLHAHSMSDKDKNSLMDLLCVMDCEEIDVDCFYYIFEAFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPLDKAIKFTERVIRYRHDISRQLYSLKTTAANVPYSNYYMYKSVFSIVMNHJTHF"
11578. .11745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYDGVHPNPLLAIQCINEKLYDKHYKIRKIAKRVIDVNCTPNVVKEVIQEVL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="ecysteroid UDP-glucosyltransferase"
/protein_id="AAN28031.1"
db_xref="G1:23476484"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10045. .11565
/note="egt; rol3; ac15-like"
/codon_start=1
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/codon_start=1
/product="unknown"
/protein_id="AAN28087.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'protein_id="AAN28161.1"
'db_xref="GI:23476614"
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/db_xref="G1:23476508"
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/db_xref="GI:23476553"
                                                                                                /note="ro10; ac12-like"
                                                                                                                                                                                                                                                                                                                                                                                                                 note="roll; ac13-like"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="unknown"
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/product="unknown"
                                                                                                                                                               /product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11711, .12388
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Best Local Similarity
Matches 124, Conserv
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VEDSFPIVNDGEWMDVFLVYNLRPTRPNRCYKFLAQHALRWDEDYVPHEVIRIVEPSY
VGMNNEYRISLAKKGGGCPLMNIHEBYTNSFESFVSRVIWENFYKPIVYIGTDSGEBE
EILIEVSLVPRVKEFAPDAPLFTGPAY"
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DIDAVVPVSKRVQNGWQIFSLINNFERETSODMLIDCLQIILGREEFKMRNGKLLELSTV
FURDNINVQWWYNKFCVVTYVHTRIMYQSVPARLAPRLSEAVKKFIRLRKSDYDDRLHL
DESYNCPRVIAEIYGRFCGIGKEHFSKHKLSCMHILFQYLRGKTTQEEESFPCYRVIK
                                                                                                                                                                                                                                                     NGGGLIKISGLRLYMLLTAPPTINEIKNSNFKKRSKANICMKECAEGKKNVVDMLNSK
INPPECIKRIGDLEKNNYPRGGMYRKRFILMCYIANVYSCAKGENRCLINALTHFYN
HDSKCVGEVMHLLIKSQDVYKPPOKOKMKNVDKLCPFAGNCKGLNPICNY"
COMPLEMENT (2429. 3064)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MAVIFNNKQLLADDSIENGGELFLINGSYSILENYVNPVLLKNG
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TWRSGTIHPIKKDIYIYDNKKFTLYDRYIYGYDNNYVNFYEEKNEKEKEYEEDDRQIK
ASSLCENKILLSQINCESFENDFKHYLDDYNYAFSIIDNSTNVLVAFGLYC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MTNRRYESVQSYLFNNRNNKIDAHQFLERVDTAEAQIIKNNIYD
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SLYNTIAYIERLLNIGTVNDSEITMLIADFYDLYSNYNIELPLPQALPRSRRPSVVQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAPADVPTIAREQTKPEQIIPTAPPPSSPASNIPAPPPPPPPPPPPSSNSELPPAPPPP
TEPEDVAPLDDRQQLLEAIRNEKNRTRLRPVKPKTVPETNTILELPTVLPKTFEPKPP
SASPPPPPPPPPPPPPPPPPPPPPPNVDLSSAPLPPPLVDLPSEMLPPPAPSLSNVLSELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGTVRLKFAQKRPQSEIIPKSSITDVLADTISRRRVAMAKSSSEATSNDEGWDDDDNR
SKAAKKEVRKYQSLFNVFTSSQLYTKNDDERWYKAHDILNDVBALLQNKTQTNIDKA
RLLLQDLASFVTLSSPNFLDSFVIGSBKQPLFTNRNLFYKSIEDLIFKFRYKEAENHL
IFALTYHPKDYKFNELLKYVQQLSVNQQRTESSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLYLQKTISAHNFNADEIKVHQLMSDHPNFIKIYFNHGSINNQVIVMDYIDCPDLFET
LQIKGELSYQLVSNIIRQLCEALNDLHKHNFIHNDIKLENVLYFEALDRVYVCDYGLC
KHENSPSVHDGTLEYFSPEKIRHYNYARSFDWYAVGVLTYKLLIGGRHPFEKSEDEML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MSLAAKLIVYNYYAKYNEVHDVYGESYHHYRIVQEYLSESYVNG"
                                                                                                                                                                                                                       'translation="MANALYNVWSPLISASCLDKKATYLIDPDDFIDKLTLTPYTVFY
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/note="consists of 30 bp imperfect palindromes; hrla;
                                                                                                                              - 2
                                                                                            /codon_start=1
/product="late expression factor
                                                                                                                                                                                                                                                                                                                                                                            /note="orf603; ro5; ac7-like"
/codon_start=1
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/note="pk-1; ro8; ac10-like"
                          1756. .2388
/note="lef-2; ro4; ac6-like"
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/note="polh; ro6; ac8-like"
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/note="orf1629; ro7; ac9"
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/product="polyhedrin"
/protein_id="AAN28081.1"
/db_xref="G1:23476534"
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/protein_id="AAN28027.1"
/db_xref="G1:23476480"
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/db_xref="G1:23476546"
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/db_xref="GI:23476522"
                                                                                                                                                           /protein_id="AAN28095.1"
/db_xref="GI:23476548"
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/db_xref="G1:23476507"
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/product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
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Ayres, M.D., Howard, S.C., Kuzio, J., Lopez-Ferber, M. and Posse
The complete DNA sequence of Autographa californica nuclear
polyhedrosis virus
Virology 202 (2), 586-605 (1994)
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Submitted (08-WAR-1999) NCBI, Bethesda, MD 20894, USA
Submitted (10-cation/Qualifiers
1. 133894
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Autographa californica nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                    unidentified
unidentified
unclassified
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Bishop, D., Possee, R. and Ayres, M.
Burdographa CaliforNica Complete Genome Sequence
Patent: WO 9601320-A 118-JAN-1996;
NATURAL ENVIRONMENT RES (GB)
other publication AU 2897295 960125.
ce
1. 133894
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/db xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="unidentified"
                                                                                                                                                                                                                A48542 1 from Patent W09601320
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L22858/c
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1 (bases 1 to 1511)
Krappa, R. and Knebel-Morsdorf, D.
Identification of the very early transcribed baculovirus gene PE-38
JU Virol. 65 (2), 805-812 (1991)
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/product = 1, inmediate-early protein PE-38"
/product = 1, inmediate-early protein PE-38"
/protein id="AAA673.1"
/db_xref="G1:332471"
/db_xref="G1:32471"
/db_xref="G1:32471
                                                                                                                                                                                                                                                   NPHPE38 1511 bp DNA linear VRL 02-AUG-1993
Autographa californica nuclear polyhedrosis virus major early
protein (PE-38) gene, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Original source text: Autographa californica nuclear polyhedrosis virus DNA, and cDNA to mRNA, isolated from Spodoptera frugiperda. Location/Qualifiers

    1511
    /organism="Autographa californica nucleopolyhedrovirus"
/mol_type="genomic DNA"
    /db_xref="taxon:46015"

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                                                                                                                                                                                                                                                                                                                                                                                    major early protein PE-38.
Autographa californica nucleopolyhedrovirus
Autographa californica nucleopolyhedrovirus
Autographa californica nucleopolyhedrovirus
Nucleopolyhedrovirus.
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                                                                                 232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAAGTACGT
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/gene="IE-N"
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/gene="PE-38"
1433. .1438
/gene="PE-38"
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352. .357
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379. 1453
/gene="PE-38"
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/procein_id="AAA66636.1"

/db_xref="G1:559075"

/db_xref="G1:55907
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PIKKDIYIYDNKKFTLYDRYIYGYDNNYNFYEEKNEKERFEEEDDKASSLCENKII
LSQINCESFENDFKYYLSDYNYAFSIIDNTTNVLVAFGLYR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product = "major occlusion body protein"

/protein id="AAA66638 1"

/db xref="G1:55907"

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MEDSFPINNOGYNUPYELVVNMFPREPREPREVKFLAGHALRCDPDYVFHDVIRIVEPREPREPREVTER

MEDSFPINNOGYNUPYELVVNMFPREPREPREVKFLAGHALRCDPDYVFHDVIRIVEPREPRESPREVTRF

MEDSFPINNOGYNUPYELVVNMFPREPREPREVTNSFEQFIDRVIWENFYKPIVYIGTDSAEEE
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/gene="Ac-ORF1629"
/note="synonym: AcOrf-9; Ac-61K; Ac-vp78"
complement(5287. .6918)
/gene="Ac-ORF1629"
/note="61K; vp78; required for virus replication; 60713 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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/translation="WTNRRYESVQSYLFNNRNNKIDAHQFFERVDTAEAQIIKNNIYD
NTVVLNRDVLLNILKLANDVFDNKAYMYVDDSEVSRHYNAVVKMKRLVIGVRDPSLRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAPAPVPTIVREQTKPEQIIPAAPPPPSPVPNIPAPPPPPPSPSNSELPPAPPMPTEP
QPAAPLDDRQQLLEAIRNEKNRTRLRPVKPKTAPETSTIVEVPTVLPKETFEPKPPSA
          SFDCNKFLRSDDMTPVVTTITPKRTADYKITEYVGDVKTIKPSNRPLVESGPLVREAA
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//gene="AG-PH"
/note="synonym: Acorf-8"
4520. .5257
//gene="AG-PH"
/note="polyhedrin; 28642 Da primary translation product"
/cote="polyhedrin; can be a primary translation product"
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/note="synonym: Acorf-7"
complement(3759, .4364)
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/note="LEF2; 23926 Da primary translation product"
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/product="late expression factor 2"
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/note="PK1; 31978 Da primary translation product"
/codon_start=1
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                                                                                                                                                                                                   'note="synonym: AcOrf-6"
                                                                                                    3089. .3721
/gene="Ac-lef2"
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VKEFTEKCPGMLVGVHCTHGINRTGYMVCRYLMHTLGIAPQEAIDRFEKARGHKIERQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /procein_id="AAA66634.1"
/db_xref="G1:559073"
/db_xref="G1:559073"
/sb_xref="G1:559073"
/scoverential physical participation of the process o
                                                                                                                                                                     sequence;
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KLPYAIELQEWLLEEVIPQVLCTGKYDPAIKQREEESKOLVTKLIATFTEHTNALQAV
VAOKTEELVKKQEFIERIVAIKDKQIEAKDLQVTRVMTDLNRMYTGFQETMQKKDEIM
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KRNINVANIVVENIRPNPTVDWNNATDRLQAKRSKRSIVLVRWKKRNNLKIG"
complement (2084. .2245)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cranslation="MQIKTVLLAFAMFAALNAQHVLAACAETGAVCVHNDECCSGACS
PIFNYCLPQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MARVKIGEFKFGEDTFNLRYVLERDQQVRFVAKDVANSLKYTVC"
                                                                                                                                                 /standard_name="hr1"
/note="5 copies of 30 bp imperfect palindromic sequence
the Ecomi site in the first palindrome is at residue 1
the linearized genome"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /notes="BRO; 37769 Da primary translation product"
/codon_start=1
/product="baculovirus repeated ORF"
/product=in_id="AAAA6632.1"
/protein_id="AAAA6632.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Da primary translation product"
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/note="12435 Da primary translation product"
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'note="17577 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                           'function="enhancer; replication origin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /porce="PTP," 19288 Da primary translation
/codon_start=1
/producie="profesin tyrosine phosphatase"
/protein_id="AAAA66631.1"
/db_xref="G1:559070"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="conotoxin-like peptide"
protein_id="AAA66633.1"
db_xref="G1:559072"
/db xref="taxon:46015"
clone="C6"
join(133883. .133894,1. .445)
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/product="AcOrf-4 peptide"
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/db_xref="G1:559074"
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/note="synonym: AcOrf-2"
complement(1041. .2027)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="synonym: Acorf-1"
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complement (2084. .2245)
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complement (2295, .2750)
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503...1009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="Ac-ptp"
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                                                                                                         repeat_region
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FVAPS PQATQTPSPRQTFAAPSPVPAESPQPTRAFPTPEGTLSRGAADEFEYFAGTSV
NGVNLNTTLKPPVPPKPAHLSRPNFMFVGDKVTGNTPPPPNGTSPQPGVNVPPPPVAP
PLNVMPPPPPPNVPPPPLDNLLLDAMMSEPRKGATDRSALFDQ1KMGATLKKAQPVE
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RSDVATSESTGFDESADTRANDKASKELKHAAHLYNFRKDSKLYNI QKVNNSELTKI
LENGPPLLKRSPRTABNUEKANGGLYLFRGHYTLPRALDAQPAPELYAADAPQFYVQ
IEDLLFPAGRYDDARAFI QAVDAPEDMKLKKPLTVANQLSTRGQ"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KHLDPLDHYMVAEDPFLGPGKNQKLTLFKEIRNVKPDTMKLIVNWSGKEFLRETWTRF
VEDSFPIVNDQEVMDVFLVINLRPTRPNRCYKFLAQHALRWDCDYVPHEVIRIVEPSY
VGMNNEYRISLAKKGGGCPIMNIHSEYTNSFESFVNRVIWENFYKPIVYIGTDSGEEE
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KQIETSCKKKKQAEERAESAALKRVELAADRMAMQAKAAPYCADDGRWSTLSQQQLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On or before Oct 8, 2003 this sequence version replaced gi:1117788,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-JUN-2003) Molecular Virology, Great Lakes Forestry Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2E5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1. .738)
/note="ORF 1; ph Op3/Ac8; major occlusion body protein"
                                                                 1 (bases 80268 to 81693)
Li,X., Lauzon,H.A., Sohi,S.S., Palli,S.R., Retnakaran,A. and Arif,B.M.
Arif,B.M.
multicapsid nucleopolyhedroviruses CfMNPV and CfDEFNPV J. Gen. Virol. 80 (Pt 7), 1833-1840 (1999)
                                                                                                                                                                                                                                                                     4 (Dases 1 to 131158)
Li,X., Barrett,J., Pang,A., Klose,R.J., Krell,P.J. and Arif,B.
Characterization of an overexpressed spindle protein during a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Choristoneura fumiferana defective
nucleopolyhedrovirus"
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Lauzon, H.A.M., Jamieson, P.B., Krell, P.J. and Arif, B.M. Direct Submission
Submitted (20-JUN-2003) Molecular Virology. Great Labe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/db_xref="taxon:74660"
join[129349. 131158,1. .20)
/note="0RF 149; 1629 capsid Op2/Ac9"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="ORF 3; lef-2 Op6/Ac6"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gi:2581770, gi:1754838, gi:4092491.
Location/Qualifiers
1. 131158
Virus Genes 13 (3), 229-237 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                product="polyhedrin"
/protein_id="AAQ91696.1"
/db_xref="GI:37499297"
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/db_xref="GI:37499343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .1220)
                                                                                                                                                                                                                                                                                                                                                                           Virology 268 (1), 56-67 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="ORF 2; Op5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (828.
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                                                                                                                                                                                                                                                                                                                                                      baculovirus infection
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TITLE
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MEDLINE
JOURNAL
                                                                         REFERENCE
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                                                                                                                                               TITLE
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               /protein id="AAA66640.1"
/db_xref="G1:559079"
/translation="MATTNATLQTLVQFYENCKNVKTRYKIINGRFGKISILSHKPTS
KLYLQKTISAHNFNADEIKVHQLMSDHPNFIKIYFNHGSINNQVIVMDYIDCPDLFFT
LQIKGELSYQLVSNITRQLCGALNDHHKHNFHNDIKLENVLYFEALDRYVVCDYGLC
KHENSLSVHDCTLEYFSPEKIFHTTMHVSFDWYAVGVLTYKLLTGGRHPFEKGEDEML
DLNSWKRRQQYNDIGVLKHVRNVNARDFVYCLTRYNIDCRLTNYKQIIKHFELS"
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Barrett,J.W., Krell,P.J. and Arif,B.M.
Characterization, sequencing and phylogeny of the ecdysteroid
UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis
viruses isolated from Choristoneura funiferana
J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The putative LEF-1 proteins from two distinct Choristoneura fumiferana multiple nucleopolyhedroviruses share domain homology to eukaryotic primases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tränslation="MSLAAKLIIYNYYAKYNEVHDVYGESYHHYRIVQEYLSESYVNG
MSCIERDVHANRILKSGSCTPDEAVKNIDAGOBIKSLSHWESYSETMATDDNVREVLE
QIDAVVPVSVYRVONGIFSLANFEREISQDMLDCLOIILGREYFRENGKLIRIANV
FNPNNDVVGWWYNKFCVVTYVHRIMYRSVPAELVPRLGSBAVKKFIRLRKSDYDDRLHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY327402 131158 bp DNA circular VRL 08-OCT-2003
Choristoneura fumiferana defective nucleopolyhedrovirus complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESYNCPRVI AEMYGR FCGIGKEHFSKHKLSCMHILFQYLRGKTTQEEKSFPCYRVIK
DFGRQCKDVYKNLKDVFDLLHAHSMSDKDKNSLMDLLCVMDCEEIDVDCFYYIFESFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CfdefnPV)
                                                                                                                                                                                                 747. 7864
'Standard name="hrla"
'note="2 copies of 30 bp imperfect palindromic sequence"
function="enhancer; replication origin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 14; Length 133894;
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Choristoneura fumiferana defective nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                        complement (7899. .8921)
/gene="AcOrf-11"
/note="40093 Da primary translation product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTACGTCGGC 278
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Pred. No. 1.2e-20;
0; Mismatches 41
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AY327402.1 GI:37499238
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/product="AcOrf-11_peptide"
/protein_id="AAA66641.1"
/db_xref="G1:559080"
                                                                                                                                                                                                                                                                                            /rpt_type=dispersed
complement(7899, .8921)
/gene="AcOrf-11"
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75.4%;
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Best Local S
Matches 126
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AUTHORS
TITLE
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AY327402
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KEYWORDS
SOURCE
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В ò g ò .

CDS

CDS

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125597 TCTACGTTTCGTAGACTATTTAACTTGAATAGTCTACACTGTTGTATACGCTCCCAATAC 125656
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                                                                                                          DPGASYFFVGEGDTYVVNGHKLAVGGYCTTNSVPRDCNRETSVVLMSLNQWTCIAEDP
FYRGYSNWTQLAGRQHFDRILDFQSDRNVLFDRLLGREVWATNTFRRSWDELLEDD
TRRFEMRCNARDNNNLMFRVNPLNPLBCLPNVCTNVNYVTSVRPPFTGECDCGDEA
VTRVRHVVPGDRSSYVCASIVDGLDTTTASREREVECVNTYTSIGNFSNNKLLCPSDTF
DSNTDAAFAFEVPGSYPLSGNGLDEPTHRFFLDTRSRIRYNDVRGLIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
/poddor=actin rearrangement inducing factor"
/protecin_id="AAO91678.1"
/db_xref="G1:37499279"
/db_xref="G1:37499279"
/db_xref="G1:37499279"
/db_xref="G1:37499279"
/db_xref="G1:37499279"
/db_xref="G1:37499279"
/db_xref="G1:37499779"
/db_xref="G1:3749979"
/db_xref="G1:3749979"
/db_xref="G1:3749979"
/db_xref="G1:3749979"
/db_xref="G1:374997"
/db_xref="
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PTPVKTLYFESAPLKEQDTADEEBEQQSSFRMLEIISEPRVQFQFPESSSLDRLSSPP
PIVQSSSSPNSPDSGIDYDIPQPFYSVPNKVVCKYLCRTHATLCA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E unimensity of the control ling an insect behavior is Kangy, v. Imai, N., Gomi, S. and Matsumoto, S. a virus in which a gene for control ling an insect behavior is Patent: JP 200324062-A 3 28-JAN-2003, THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH OS Bombyx mori nucleopolyhedrovirus PP 28-JAN-2003 PP 10-JUL-2001 JP 2003024062-A/3 PP 10-JUL-2001 JP 2003024062-A/3 OF INSUMIKO GOMI, SHOGO MATSUMOTO PC CI2N15/09, A01K67/033, CI2N7/04 SmNPV genome DNA FH Key Incontrol Logation/Oualifiers

FT source 1.28413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 100; DB 14;
Pred. No. 3.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        7898. .8863
/note="ORF 11; arif Op19/Ac21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (9013. 9327)
/note="ORF 12; Op18/Ac19"
/codon_start=1
       note="ORF 10; Op20/Ac20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="unknown"
/protein_id="AAQ91753.1"
/db_xref="G1:37499354"
                                           /codon_start=1
/product="unknown"
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BD187790.1 GI:32997529
JP 2003024062-A/3.
unidentified
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80.6%;
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Best Local Similarity
Matches 129; Conserv
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BD187790/c
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TITLE
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EINCHAPLETRGASRVQAFFALDSLEFPPNMTDSLQVLMGRFMHFVRGYALTHVANVF
DPTIKLDGWWYNKFCVLTYMYRIIRGTVPAELITRLQNVVTKYIKPEYDESNNALAMG
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LPYAVELQENLLEEVIPQVLCTGKYNPAIKQQDEBKKQLINKLVKTFSDHTWTLQTAL
LQCYQELVKKQSFIERIVATKDKQIEBKDLQVTRVWTDLNRWYNGFQETWQKKDEIMQ
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RNLSAADIVAETTRPNPTVDWNNATHRLAAKKSKRTISFDSEQDAQQPATRIKQLLN
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location similar to Ac hria"
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TSCVRRDIETARRLNRGELSFDDARRQLNLEEIAKRLATWYHTGEMKSFCSEIQSVLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DIQLQVDILHSHAMTDKQKNALFDLLCCNNASDIDVDCYDYIVKKFYNIAVY"
                                                                                                                                                                                        EVTHLLIKAEDVYKPSNCAKMKTVNKLCPKAGMCKGKNPICNF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (3686. .4168)
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/codon start=1
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'note="ORF 9; Op11/Ac11"
                                                                                                                                                                                                                            complement (1861, .2124)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2171. .2608
/note="ORF 5; Op8/Ac4"
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protein_id="AAQ91716.
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OPAAPAPVPTIVHEQTKFEQIIIPAAPPPFSSVPNIPAPPPPPPPSSMSELPPAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MPTKPQPAAPLDDRQQLLEAIRNEKNRTRLRPVKPKTAPETNTIIEVPTTVLPKEPKP
SASSPPEPPEPPPARPAPPHDLSSAELQPPULDLAFAKMPPPPARSLSNVLSELKSGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTSKLYLQKTISAHNFNVDEIKVHQLMNDHPNFIKIYFNHGFINNQVIVMDYIDCPDL
FETLDIKGELSHQLVSNIIRQLCEALNDLHKHNFIHNDIKLENVLYFERLDRVYVCDY
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EMLDLNSMKRRQVRDIGVLKHVRNVNARDFVYCLTRYNLDCRLTNYKQIIKHEFLS-
COMPLEMENT (3248. , 4270)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENPNSDAVGWWYNKFCVITYVHRIMHRSVPAELVPRISEAVKKFIRLSKSDYDDRLHV
DESYNCPRVIAEMYGRFCGIGKEHFSKHKLSCMHILPQYLRGKTTQEEKSFSCYTVIK
DFGRQCIDVYRDLKDVFDLLHAHSMSDKDKNSLMDLLCVMDCEEIDVDCFYYIFESFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAC63687.1"
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HLIBIIFHKQKSKRDLNSLGALFATKQGLLKILMRLNFDNSGNALLHLQTEGRRDDLR
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VEDSFPIVNDQEVMDVYLVANLKPTRPNRCYKFLAQHALRWEEDYVPHEVIRIVEPSY
VGMNNBYRISLAKKGGGCPIMNIHSEYTNSFESFVNRVIWENFYKPIVYIGTDSAEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLLLQDLASRVVLSENPLDSPAĪGLQKQPLFETNRNLFYKSIEDLIFKFRYKDAENHL
IFALTYHPKDYKFNELLKYVQQLSVNQQRTESNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MATTTATNATLQTLVQFYENCKNVKTRYK1INGRFGKISILSHK/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MSCI ERDVTAMRRLKI GSCTFDEAVKM I DAGDSI KSLSHWFSTGETTGI DDNVRKVLE
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complement (768. 2396)
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complement[4605. .5600)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  22171 CTACAAATCGTAGACTATTTTATTAGAATAGTCTACAGTACTATACGCTCTCAATAA 22112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequencing of the putative DNA helicase-encoding gene of the Bombyx mori nuclear polyhedrosis virus and fine-mapping of a region involved in host range expansion Gene 190 (1), 173-179 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gomi, S., Majima, K. and Maeda, S. Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus J. Gen. Virol. 80 (Pt 5), 1323-1337 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bombyx mori nuclear polyhedrosis virus isolate T3, complete genome.
L33180
                                                                                                                                                                                                                                                                                                     171
                                                                                                                                                                                                                                                                                                                                                                                                   172 CTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (14-0CT-1998) Laboratory of Molecular Entomology and Baculovirology, The Institute of Physical and Chemical Research (RIKEN), Hirosawa 2-1, Wako 351-0198, Japan Sequence update by submitter on Oct 14, 1998 this sequence version replaced gi:1196668.

Location/Qualifiers
1. 128413
//organism="Bombyx mori nucleopolyhedrovirus"/mol type="genomic DNA"/isolate="T3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-MAY-1994) Department of Entomology, University of California, Davis, CA 95616, USA (bases 1 to 128413)
                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
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9
                                                                                                                                                                                                 Score 93.4; DB 6;
Pred. No. 3.2e-18;
0; Mismatches 46
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                                               1. .28413
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Bombyx mori nucleopolyhedrovirus
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                          Location/Qualifiers
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Kamita, S.G. and Maeda, S.
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LOCUS

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5 (bases 1 to 129609)
Qiu, w. thu, J. and Carstens, E.B.
Studies of Choristoneura fumiferana nuclear polyhedrosis virus
expression in insect cells
                                                                                                                                                                                 46;
                                                                                                                                                               Pred. No. 4.5e
0; Mismatches
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Virology 209 (2), 409-419 (1995)
95297142
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                                     /trānslation="MLLCNYTQKRVDMMDAIAYNDSRKYAFMTVNARWIHADKYFDT
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FAHCVREAVRLYIFMHQDSNLDALTLQYWPDVDRDIFCNVNKQIRAPYSYNYKGTKKF
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                                                                                                                                                                                                                                                                                                                                                                                                                        LSPVĪDAKNNKSKSGAIYVSFGSSIDTKSFANEFFYMLINTFKALDNYTILWKIDDEV
VONTILPANVITQNWFNORAVIRHKKWAAFITQGGLQSSDBALBAGIPWVCLPMMGDQ
FYHAHKLQQLGVARALDTVTVSSDQLILAINDVLFNASTYKKHMAELYALINNDKATF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAKEKVLIIVDGFDSAYIQATFCSISDSVTIVNKFNEKHVMFDGFVRPDDEGTTMPY
VICPPLSVDAAVADRKVKDMYNSIENQQTMLKVFINEANVYNKMNMLKGLIYNNNNB
SVLVNNVVKFIKVDRVXNVTKKNNVTKWVPAVNYFTGRQLLTILFIFKFK"
complement (9387. . 10457)
                                                                                                                                                                                                                                                                                                                                        EKCHNVTVVKPKLFAYSTKTYCGNITEVNSDMSVKQYKKLVTNSAMFRKRGVVSDTDT
YTAANYCLE LEMFKOOFDNINVRNITANNGTFDLVVVBAFADYALVEGHYDPBAVIO
1APGYGLARNFDTVGAVARHPVHPNIMRNNFDDTKANLMTEMLYKEFKILANMSNA
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DRYHULVSZLQRVLNDQLMCLLKDIFNKFDYKIKRRLNHLKRLFANLDAESYNSCVN
YPHKNLCDQNWRRFNSCIFSLY"
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Xie,W.D., Arif,B., Dobos,P. and Krell,P.J.
Identification and analysis of a putative origin of DNA replication in the Choristoneura funiferana multinucleocapsid nuclear
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                                                                                                                                                                                                                                                                                                                                                                                                          CTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
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Choristoneura fumiferana MNPV
Choristoneura fumiferana MNPV
Viruses; daDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
1 (bases 1 to 12560)
Lee, H. Y., Arif, B., Dobos, P. and Krell, P.
Identification of bent DNA and ARS fragments in the choristoneura fumiferana nuclear polyhedrosis virus Res. 24 (3), 249-264 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAAGTACGTGTCGGC
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PHTVLINNNYAQDAFQFAI."
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VDEFODRCPTMLVGVHCTHGINRSGYLVCRYMVDKLGVSPADAIIRFEEARGHKIERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(3738. .4220)
//octe="ORTR8; ptp2; Op9"
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GQWSKLTSAQLDEIAREKDIVDRIYQLQLKQDRLIKMDGLKKQ"
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SAALVVYYYMRSRQMSYEEALSLVKNKRRVAISNHFVRFLASKCSYKFVNNVLKIRVS
                                                     complement (1251. .1859)
/note="ORF3; lef2; Ac6/Op6"
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/note="ORF7; Ac136/Op132"
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/note="ORF10; Ac11/Op11"
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/note="ORF5; Ac4/Op8"
                                                                                                                                                                                                                                                                                                                                    /note="ORF4; Ac5/Op7"/codon_start=1
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product="unknown"
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/note="ORF6;Ac2"
                                                          complement (1251.
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Lappinte, R., Back, D.W., Ding, Q. and Carstens, B.B.
Lappinte, R., Back, D.W., Ding, Q. and Carstens, B.B.
Identification and molecular characterization of the Choristoneura
Identification and molecular characterization of the Choristoneura
Itumiferana multicapsid nucleopolyhedrovirus genomic region encoding
the regularcry genes pkip, p47, lef-12, and gta
Virology 271 (1), 109-121 (2000)
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/protein_id="nAP229795.1"
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EDSPPIVNDQEVMDVFLVVNMRPTRPNRCYKFLRQHALRWDCDYVPHEVIRIVBPSYV
GMNNEYRISLAKKGGGCPIMNIHAEYTNSFESFVNRVIWENFYKPIVVIGTDSGEEEE
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GRHKVVPKSKHVQGLESNLQLLVGVSKHGKMAASDQKILELFYRWSSQTGCEMLDDEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (13-MAY-2002) Department of Microbiology, University of Guelph, Chemistry and Microbiology Building, Guelph, ON NIG 2W1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carstens, E.B., Liu, J.J. and Dominy, C. Identification and molecular characterization of the baculovirus GENBY early genes: ie-1, ie-2 and pe38 Virus Res. 83 (1-2), 13-30 (2002)
                                                                                                   Liu, J.J. and Carstens, E.B. Identification, molecular cloning, and transcription analysis of the Choristoneura fumiferana nuclear polyhedrosis virus
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de Jong, J.G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B.
and Krell, P.J.
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de Jong,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B.
and Krell,P.J.
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de Jong, J. G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B.
and Krell, P.J.
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On May 13, 2004 this sequence version replaced gi:30269978
Location/Qualifiers
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complement (838. .1449)
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Virology 217 (2), 564-572 (1996)
96183379
                                                                                                                                                                                   spindle-like protein gene
Virology 223 (2), 396-400 (1996)
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/note="ORF1; Ac8/Op3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2178 bp DNA linear VRL 03-FEB-1999 Bombyx mori nuclear polyhedrosis virus genes for BmIE-N and BmPE36, partial cds and complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (18-FEB-1993) Gentaro Yamamoto, Nagoya University Faculty of Agriculture, Dept. of Agricultural Chemistry; Nagoya, Aichi 464-01, Japan (Tel:052-781-5111(ex.6238), Fax:052-781-4447) Submitted (18-FEB-1993) to DDBJ by:
                                                                                                                                                                                                                                                                                                     CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
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                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                               16.3%; Score 92.2; DB 14; Length 129609; 78.3%; Pred. No. 1.1e-17;
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/organism="Bombyx mori nucleopolyhedrovirus"
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BmIE-N; BmPE356; immediate-early gene.
Bombyx mori nucleopolyhedrovirus
Bombyx mori nucleopolyhedrovirus
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complement(<1. .414)
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                                                                                                                                                                       complement (5854. .6387)
xref="GI:30269988"
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                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                            ÷
                                                                                                                                                                                    16.3%; Score 92; DB 14; Length 2178; 72.6%; Pred. No. 5.3e-18;
                                                                                                                                                                                                                                                                                                                            CCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGGC 278
                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                            45;
                                                                                                                                                                                                            0; Mismatches
                                                       /protein_id="BAA03364.1"
/db_xref="GI:222186"
                                                                                                                                                                                                                                                                                                                                                                                  rch completed: October 24, 2005, 20:17:59 time: 3425.8 secs
.493)
                                              /product="BmPE36"
complement (487.
                                   /codon_start=1
            .788
                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                Best Local Similarity
Matches 119; Conserv
                                                                                                                                          polyA_signal
ORIGIN
TATA_signal
TATA_signal
CDS
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                                                                                                                                                                                                                                                                                                                                                   592
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Run on:

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VERSION
KEYWORDS
SOURCE
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TITLE
JOURNAL
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AV398660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
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N63392 Y235H10.81
BZ990283 CH240_23B
BZ899636 CH240_16P
CC3410241 NISC_nc10
CC384338 AGENGOURT
AL065938 Drosophil
A1477474 Eb34506.x
B1842287 Et59f05.x
CR709617 Tetraodon
CC955894 MBEANOSTR
BH757407 SALK_0561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV398660 AV398660
CL077394 CH216-145
BX1477578 Danio rer
CG751412 P045-4-E0
BH517933 BOGBL87TF
                                                                                                                                                                                                          ; Search time 4071.35 Seconds (without alignments) 5273.001 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                 1 catgatgataaacaatgtat.....tgttacagcgacacaacatg 564
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                         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34239544 segs, 19032134700 residues
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                                                                                                                                                                                                          October 24, 2005, 18:41:23;
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                                                                                                                                                nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
Listing first 45 su
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seq length: 200000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
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Minimum DB Maximum DB

Database

Searched:

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Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Lepidoptera; Glossata; Dirrysia;
Bombycoidea; Bombycidae; Bombyx.

1 (bases 1 to 679)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Agrobiological Sciences
Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan
Email: Kmita@niaa.affrc.go.jp
method:uni-directional, sequence direction:sequenced from T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 05-FEB-2000
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                                                                                 HS 5574 B
ZF101-P00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV398660 Bombyx mori ovary BmNPV infected; 6 hr after inoculation Bombyx mori cDNA clone NV060140 T3, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="ovary"
/cell_type="mmw cultured cell"
/dev_stage="mmwpw infected; 6 hr after inoculation"
/clone_lib="mombyx mori ovary mnNFW infected; 6 hr after
inoculation"
                                                                                                                                                                                                                                                                                                                           Drosophil
ID0AAA15D
                                                                                                                                                                                                                                                                                                                                                                                                                  ENTPM01TF
CH213-86H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                     AL188860 7
AQ751255 F
CK706618 2
CG020891 2
CC847625 F
AL068607 F
BM525801 8
                                                                                                                                                                                                                                                                                            AG394612 NAL062985 UCN755468 UCN80859 BH150387 UCL645025 CE275017 AL259808 UCL089685 UCCS78872 UCL089685 U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
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/mol_type="mRNA"
/db_xref="taxon:7091"
/clone="NV060140"
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Bombyx mori
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BH150387
CL645025
CE275017
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BG247625
CNS00LO0
BM525801
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CNS0067B
CN755468
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CG578872
                               AQ857977
CNS02APV
                                                                                                                   CK706618
CG020891
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Best Local
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BE374425 601227596 CL510716 SAIL 836 BM278655 As tg2_65 CL753134 OR BBa012 AG401197 MUS muscu

BM278655 CL753134 AG401197

BE374425 CL510716

675 715 1049 516 613

AG358704

CR709617 CG935894

Result

CB484581

BH757407 SALK 0561 AG358704 Mus muscu

BG695019 NISC .

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VERSION
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AUTHORS
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COMMENT
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AUTHORS
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CG751412
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Danio rerio genomic clone DKEY-109J14, genomic survey sequence.
BX147578
                                                                                                                                                                                                  GSS 31-DEC-2003
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                 61 TITTATTAGAATAGTCTACACTGTACTATACGCTCTCAATATACTACTACTACAATTTAGAATATACAACTACAACT 120
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                                                                                                                                                                                                                                                                                            Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Xenopus tropicalis
Anuacia, Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

(Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                               CH216-145B11_Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-145B11, genomic survey sequence.
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52.4%; Pred. No. 0.48;
ive 0; Mismatches 79; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 ATAACGATATTACCACTCACTCACTCCTTCTGTACCCATATAAATT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAAATACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAGT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 175000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Xenopus tropicalis"
/mol_type="genomic DNA"
/strain="Nigerian frog"
/db_xref="caxon:8164"
/clone="CH216-145B11"
                                                                                                   121 TTTTGCATTACAAAAAGTTCATTTTGC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence start: 163
High quality sequence scop: 226.
Location/Qualifiers
1. 954
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Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

I (bases 1 to 762)

Humphray, S.J., Huckle, E. and Durham, J.L.

Direct Submission

Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CBIO 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bases 1 to 1324)
Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perebolte, L., Jansen, K., Buntjer, J., van der Meulen, M. and Sommer, R.J.
An integrated physical and genetic map of the nematode Pristionchus pacificus
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                                                                                                                                                                                                                                                                                                                                                                     This sequence was generated from the T7 end of BAC 109J14. 109J14 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 TACGCTCCAAATACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCG 276
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Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
Neodiplogasteridae; Pristionchus.
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Max-Planck-Institute for Developmental Biology
Spenannetr. 37-39, Tuebingen D-72076, Germany
Tel: 0049707160139,
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/D_rerio/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-109014"
/issue_type="Testis"
/note="Vector pIndigoBAC-536"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Danio rerio"
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CG751412.1 GI:37973841
BX147578.1 GI:27978953
                                                      Danio rerio (zebrafish)
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6.8%;
49.2%;
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Best Local Similarity 49.29
Matches 97; Conservative
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AUTHORS
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BOGBL87TF BOGB Brassica oleracea genomic clone BOGBL87, genomic
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                                                                                                                                                                                                                                                                           1092 AATATCACCACCTTTTTAATCTTTTTTTTTTTTTTTTGAAACCCCCTTTTTTAACCCTCC 1151
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                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                           98 GCCTCCCCACCACCACATTTTTGCACTGCAAAAAAAACACGCTTTTGCACGCGGCCCCAT 157
                                                                                                                                                                                                                                                                                                                                                                               158 ACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTAT 217
                                                                                                                                                                                                                                        AACAACAATTCTGTTGAACTGTTTTTCATGTTTGCCAACAAGCACCTTTATACTCGGTG 97
                                              /db.xref="taxon:54126"
/dlone lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genemic DNA with EcoRI and cloning into the BAC
vector."
                                                                                                                                                                                                           Gaps
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 ACCCTCCAAATACACTACCACATTGAACCTTTTTGCAGTGCAAAAAGT 268
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52.1%; Pred. No. 0.95;
iive 0; Mismatches 79; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="BOGB"
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb
genomic DNA inserted into pHOS1 using BstXI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11: cdtown@tigr.org
is from a doubled haploid provided by Tom Osborn.
primer: TF
                                                                                                                                                                    Score 39; DB 9; Length 1324;
Pred. No. 0.81;
0; Mismatches 120; Indels
   pacificus"
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/organism="Pristionchus
/mol_type="genomic DNA"
/strain="California"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA'
/strain="TO1000DH3"
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BH517933.1 GI:17726023
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Seq primer: TF
Class: sheared ends.
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                                                                                                                                                                                                         111; Conservative
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Fax: 301-838-0208
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Brassica oleracea
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Best Local Similarity
Matches 86; Conserv
                                                                                                                                                                       Query Match
Best Local
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ORGANISM
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BH517933/c
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1 (bases I to 535)

1 (bases I to 535)

1 (bases I to 535)

Chispoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, M., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Le, N., Te, M., Le, N., Prands, E., Mocre, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevakkis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R.
                                                                                                                                                           Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: ml3 -40 forward
High quality sequence stop: 246.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 ATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGT
                                                   527 CCAGTTGGTTTGCACTTTACAAGATTAATGATCAGTACTCTCATCAACAAATATTATAAA
                                                                                                       CTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATA
CCAACTITITIGCACTGCAAAAAACACGCTTTTTGCACGCGGGCCCATACTAGTACAAA
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0
                                                                                                                                                                                                                                                                                                                                                                                                    N63392 535 bp mRNA linear EST yz35h10.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:285091 3', mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                 AAATTCAATACAATTAAATATGTAAAAAATAAAATTAGACATTT 363
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Pred. No. 1.2;
0; Mismatches 100;
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/db_xref="GDB:3892208"
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/clone="IMAGE:285091"
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                                                                                                                                                                   252 CATGCTGATCAATGAGGCATAAAGATATAATTGGTTTATAGACACACATTTGTTGGAATGTA 193
                                                                                                                                                                                                                               61 TTTTCATGTTTGCCAACAAGCACTTTATACTCGGTGGCCTCCCCACCACCTTTTTT 120
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia: Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                       Gaps
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                                    Indels
                                    90 ;
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      Pred. No. 1.4;
0; Mismatches
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/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_16P5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Bos taurus"
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1. .582
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      Local Similarity 55.2%;
tes 74; Conservative
                                                                                                                                                                                                                                                                                                                                                          121 GCACTGCAAAAAA 134
                                                                                                                                                                                                                                                                                                                                                                                                                             132 TCAGCATTAAAAA 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovinae, Bos.
1 (bases 1 to 582)
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Other_GSSS: CH20_3183.TV

Contact: Harris Lewin

Department of Animal Sciences

University of Illinois at Urbana (Lemon Champaign

1201 W. Gregory Dr., Urbana, IL 61801, USA

Tel: 217 333 5998

Fax: 217 244 5617

Email: h-lewinchuic.edu

Clones are derived from the bovine BAC library CHORI-240

(http://www.chori.org/bacpac/bovine240.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/ordering_information.htm). This work

was undertaken as part of the International Bovine BAC Mapping

Consortium (IBBMC) by by University of Illinois at Urbana

Champaign, USA with funds provided by grant No. AG202-34480-11828

from USDA-CSREBS and A639-35205-8534 from USDA/NRI (Livestock

Genome Sequencing Initiative)

Plate: 23 row: B column: 3

Seq primer: SP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Larkin, D.M., Everts-van der Wind, A., Rebeiz, M., Schweitzer, P., Bachman, S., Campos, E.J., Benson, L.D., Edwards, J., Liu, L., Womack, J.E., de Jong, P.J. and Lewin, H.A. A Cattle-Human Comparative Map Built with Cattle BAC-ends and Human
ATACGCTCCAAATACACTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTACGTGTC 275
                                                                                                                                                                                                                               GGCAGTCACGTAGGCCGGCCTTATCGGGTCGCGTCCTGTCACGTACGAATCACATTATCG 335
                                                                                                                                                               ATTTGCCCAAATTTCACCAGGTTTTACTTAAAAATTCTACCTTATGGGTAAATACCAGGC 337
                                                                                                                                                                                                                                                                                              Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone_lib="CHOR1-240"
/note="Vector: pTARBAC1.3; Site_1: Mbol; Site_2: Mbol;
Hareford blomino 99375; CHOR1-240 Bovine BAC
library (Male) produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic_DNA"
/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH40_23B3"
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1. .578
/organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                             GACCGGACGAGTGTTGT 352
                                                                                                                                                                                                                                                                                                                                                                                                                      GACNGGATAAATNATTT 414
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1 (bases 1 to 578)
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TITLE

COMMENT

Best Local Similarity

6.7%; Score 38; DB 8; Length 578;

Query Match

ORIGIN

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/lab hose="YPOP10"
//lab hose="YPOP10"
//lote="Organ: with property to the property of the pro
       126 TTTTTGATGCAATATATTTGCCAAAAAACTCAGCTTTTATTTTCCATTTTAAACAACTA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Ambhlbia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Xenopodinae, Xenopus, Xenopus.

1 (bases 1 to 669)

1 (bases 1 to 669)

Nath-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              National Cancer Institute / NIH
Bidg. 31 Rm10A07 Bethesda, MD 20892
Enail: gapbs=r@mail.nih.gov
Tissue Procurement: Blumberg
CDNA Library Preparation: B. Blumberg
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM15322 row: j column: 11
High quality sequence stop: 534.
                                                                                                                                                                                                                                                                                                                  CO384338 16189343 Blumberg Cho dorsal blastopore lip Xenopus laevis CDNA clone IMAGE:7297357 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.6%; Score 37.2; DB 7; Length 669; 57.9%; Pred. No. 2.6; tive 0; Mismatches 48; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tissue_type="dorsal blastopore lip"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xenopus laevis (African clawed frog)
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:7297357"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                          186 CAATATTACAAGCTGTT 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CO384338.1 GI:49490161
                                                                        235 CCACACATTGAACCTTTT
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CO384338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NISC_nc10d09.x1 COGENE 6E MAX Homo sapiens cDNA clone IMAGE:57765533', mRNA sequence.
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/note="Vector: pAMP1; cDNA_primed using oligo-dT primer,
/note="Vector: pAMP1; cDNA_primed using oligo-dT primer,
/note="Vector: pamP1; cDNA_primed using oligo-dT primer,
selected for insert sizes ranging from 0.2-1.8 kb.
Normalized to Cot5. Primary library, non-amplified.
Library constructed by M. Lovett. For more information on
University) or visit the COGENE_NT indeel (Washington
University) or visit the COGENE_website at
http://hg.wustl.edu/COGENE_Website at
                                                                                                                                                                                                        61 TITITCATGITIGCCAACAAGCACCITIATACTCGGTGGCCTCCCCACCACCACTTTTT 120
                                                                                                                                   265 cargeridarcaargacgeraraagaraarraggriraragacacarrrightiggaargra 324
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I (Dases I to 425)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NALI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation:
                                                                     1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
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   0; Gaps
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llarity 54.3%; Pred. No. 2.3;
Conservative 0; Mismatches 63; Indels (
   60; Indels
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/dev_stage="6 weeks postconception"
/lab_host="DH108"
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:5776553"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB410241.1 GI:29166981
                                                                                                                                                                                                                                                                                                                                                   121 GCACTGCAAAAAA 134
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74; Conservative
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EST Danio rerio cDNA clone
  mRNA
432 bp
fbb4b06.x1 Zebrafish WashU MPIMG
MAGE:3713747 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 423 POLYA=No.
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/db_xref="taxon:7955"
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                                                                                                          AI437474.1 GI:4286113
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Best Local Similarity
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                                                                                                                                                                                          Danio rerio
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                                                                                                                                                            SOURCE
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Direct Submission

Submitted (12-JUN-1999) Genoscope - Centre National de Sequencage:

BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Osoegawa and Marmoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                               03-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133 AACACGCTTTTGCACGCGGCCCATACATAGTACAAACTCTACGTTTCGTAGACTATTTT 192
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  CCCATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAATAGTCTACACCGT 212
                                                                                                                                                                                                                                                                                          CNS0039X 1101 bp DNA linear GSS 03-JUN-15
Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR08012 of RPC1-98 library from Drosophila melanogaster (fruit
                                                 104 CCAATAAATAGGGGAACCTTCTGGTATAGTTGTAAAGAATACATCCAATGTATGCAACGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophila.
1 (bases 1 to 1101)
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/mol type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR08012"
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                                                                                                                                                                                                                                                                                                                                                            fly), genomic survey sequence. AL063938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="RPCI-98"
/note="end : T7"
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AJ437474
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TITLE JOURNAL

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AUTHORS

REFERENCE

ACCESSION

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Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4442 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. CDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@esgen.com) and
RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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1 (Dases 1 to 432)
Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,O., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M. Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Riter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Washu Zebrafish BST Project 1998
Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="26 somite embryos, adult livers, shield stage embryos"
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CB484581 480 bp mRNA linear EST 01-APR-2003 ccluwtbh009074 Coregonus clupeaformis head Coregonus clupeaformis cDAA, mRNA sequence.
CB484581. GI:29295807
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(bases 1 to 1048)
                                                                                                                                                                                                                    87 AGTGAACAATTTACAAATATATAAAACAACAACTGTTTTCTGTTGCTACTAAGCACTT 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (10-AUG-2004) Genoscope - Centre National de Sequencage : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE CREmail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
More information available at http://www.genoscope.cns.fr/tetraodon.
Location/Qualifiers
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                                                           27 ATCACTITIATITICCTACTGTACAGCGTGAATITITIACTTTTGCAAAGTGACAAAACTG
                                                                                                                                                                 169 ACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAAT
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                                                                                                                                                                                                                                                                             229 ACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGGCA 279
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     84; Indels
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Tetraodon nigroviridis
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Pred. No. 4.5;
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/db_xref="taxon:99883"
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="Organ: ovary (pooled); Vector: pBluescript SK-;
Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolatd from
the ovaries of 2 female adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into
lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
mass-excised to pBluescript SK- following the Washington
                                                                                                                                                                                                                                                                                                                                                                                  EST 04-OCT-2001
                                                                                  169 ACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAAT 228
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Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clark M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theigh, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Matter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Washu Zebrafish EST Project 1998
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Actinopterygii, Neopterygii, Teleostei, Ostariophysi, Cypriniformes; Cyprinidae, Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
                                                                                                                                     81 AGTGAACAATTTACAAATATATAAACAACAACAACTGTTTTCTGTTGGCTACTAAGCACTT
                                                                                                                                                                                          229 ACACTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTACGTGTCGGCA 279
                                                                                                                                                                                                                                           141 ACTCTACTACACTTCAATTACACGGAGAGCCTAAAAGTACATGACAAA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                      ft59f05.x1 Gong zebrafish ovary Danio rerio cDNA clone
IMAGE:5157656 3', mRNA sequence.
B1843287
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50.9%; Pred. No. 3.9;
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′organism="Danio rerio"
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/db_xref="taxon:7955"
/clone="IMAGE:5157656"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI843287.1 GI:15955810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danio rerio (zebrafish)
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Best Local Similarity
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TITLE

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FEATURES

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Gaps

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Indels

Length 1048;

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GRASP CONSOrtium, Davidson, W.S., Koop, B.F. and http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA libraries
Libraries
Lumpublished (2002)
Contract: Koop BF
Contract: Koop BF
Contractisty of Victoria BC, V8W 3NS, Canada PO Box 3020 STN CSC, Victoria BC, V8W 3NS, Canada Tal: 250 472 4075
Email: bkoop@uvic.ca
Centre for Biomedical Research, University of Victoria cDNA preparation and sequencing: Roberto Alberto, Marianne Beetz-Sargent, Maura Busby, Peter Hunt, Linda McKinnel, BF Koop.
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EST.
Coregonus clupeaformis
Coregonus clupeaformis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metypai; Peopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Coregonus.
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7. .crganism=".coregonus clupeaformis"
/mol_type="mRNA"
/db_xref="taxon:59861"
/clone lib="Coregonus clupeaformis head"
/clone="Wector: pBlueScriptIISK+; Library Creator:
/kristian R von Schalburg ; Lake whitefish tissue
contributor: Louis Bernatchez (Universite Laval)"
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Expression vectors for transforming insect cells from disparate lines useful to express heterologous DNA, e.g. to allow study of gene expression and produce commercially important proteins.

WPI; 1998-557129/47.

This represents a Orgyia pseudotsugata multicapsid nucleopolyhedrosis virus (OpMNPV) immediate early 2 (Op ie2) promoter sequence. The invention provides a new shuttle vector for transforming insect cells

ABL19380 AAS18541

AAV34232 ACD08103

Claim 10; Page 82; 121pp; English.

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             promoter having homology to, and capable of functioning as, an immediate early baculovirus promoter; (iii) prokaryotic promoter sequence, and (iv) selectable marker capable of conferring resistance to a bleomycin/phleomycin-type antibiotic under transcriptional control of (ii) and (iii), in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) cells with heterologous DNA, useful to allow study of gene expression and direct expression of heterologous gene products e.g. commercially important proteins. They are especially useful to allow expression of the heterologous
                                                                                                                                                                            melanotransferrins, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transfermation of insect cell lines from disparate species, allowing screening of lines for optimum post-translational modification of particular proteins. Shuttle vectors (further comprising DNA transposable elements defining a transposon can be used to optimise heterologous protein expression and facilitate selection of desired transformants. (Updated on 17-OCT-2003 to standardise os
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replication; (ii) insect
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                                                                                                                                                                                                                                                                                                                                             Sequence 564 BP; 147 A; 160 C; 116 G; 141 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 564; DB 2; I 100.0%; Pred. No. 1.1e-172;
                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
prokaryotic origin of
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Matches 564; Conservative
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Best Local 8
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BP

ADQ48575 standard; DNA; 560

RESULT 2 ADQ48575 (first entry)

09-SEP-2004

ADQ48575;

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The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful for producing and expressing fusion polypeptides. The present DNA sequence represents the OpIE2 promoter that was used in the present.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                replication-defective particle generation; gene expression inhibition;
gene therapy vector; ds; OpIB2 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAACAATTCTGTTGAACTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.2%; Score 54%; DB 12; Length 560; 100.0%; Pred. No. 1.8e-167; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 560 BP; 144 A; 156 C; 116 G; 144 T; 0 U; 0 Other;
                                                viral vector; recombination site; recombinant virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harwood S, Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Fig 16; 555pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the invention.
                                                                                                                                                                                                                                                    18-JUL-2002; 2002US-0396335P.
26-JUL-2002; 2002US-039647PP.
19-NOV-2002; 2002US-042731P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
                                                                                                                                                                                                                     18-JUL-2003; 2003WO-US022437
              OpIE2 promoter DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.'
Matches 548; Conservative
                                                                                                                                                                                                                                                                                                                                                         INVITROGEN CORP
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                                                                                                                                                                                                                                                                                                                                                                       BENNETT R P. WELCH P J. HARWOOD S.
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                                                                                                                                                                                                                                                                                                                                                                                                                         MADDEN K.
FRIMPONG K.
FRANKE K E.
                                                                                                                                                   WO2004009768-A2
                                                                                                                   Unidentified
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(HARW/)
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gene therapy. The present sequence is p220p2F expression vector insect cells. This sequence is used to illustrate the method of
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              insect ce]
invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to immunogenic analogues of multimeric proteins such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis factor alpha (TNF, TNFalpha) and methods for production of immunogenic analogues. The immunogenic analogue is useful for preparing a composition for treating inflammatory diseases, e.g., arthritis. It is also used in
                                                                    364
                                                                                                           GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 420
                                                                                                                    365 GACAGGACGACCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 424
                                                                                                                                                GGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC 480
                                                                                                                                                         425 GGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCC 484
                                                                                                                                                                                                485 GTCCCGCTTATCGCGCCTATAAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New immunogenic analogue of a polymeric protein, useful for preparing a composition for treating inflammatory diseases e.g. arthritis.
                                                                                                                                                                                                                                                                                                                                                                          Multimeric protein; interleukin 5; IL5; TNPalpha; inflammatory disease;
tumour necrosis factor alpha; gene therapy; arthritis; gene; ds.
                                                                               GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
                               GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouritsen S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Voldborg B,
                                                                                                                                                                                                                                                                                                                                                         p2ZOp2F expression vector for insect cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bratt T,
                                                                                                                                                                                                                                                                                               AAL61306 standard; DNA; 2773 BP.
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16-NOV-2001; 2001US-0331575P.
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NIELSEN F S.
BRATT T.
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                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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(BRAT/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAGGTTGAACAGGTTGAACAGGTTGAACAGGTTCTGATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
                                                                                                                                                                                                                                                                                                                          185 GTAGACTATTTTACATAAATAGTCTACACGTTGTATACGCTCCAAATACACTACACACA
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                                                                                                                           1 CATGATGATAAACAATGTATGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                        CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                 TITICATGITIGCCAACAAGCACCITIATACTCGGTGGCCTCCCCACCACCATTTTT
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                                                                                     Gaps
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0
                                          Length 2773;
Sequence 2773 BP; 669 A; 750 C; 673 G; 681 T; 0 U; 0 Other;
                                                                                   Indels
                                      97.2%; Score 548; DB 9; Le
100.0%; Pred. No. 3.8e-167;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viral vector-related plasmid - pIB/V5-His-DEST.
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                                                              Best Local Similarity 100.
Matches 548; Conservative
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GGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Possee R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1996-087670/09
                                                                                                                                                                541 CATCTGTT
                                                                                                                                                                                                        541 CATCTGTT
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                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2003
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      421
                                                                                                                                                                                                                                                                                                                                                   AAT13730;
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                                                                                                                                                                                                                                                                                     AAT13730/c
                                                                                                                                                                                                                                                                  RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention replication of executions are recombinant virus, generating replication-defective particles, and are useful for expression of one or more genes in an organism, and are useful for producing and expressing fusion polypeptides. The present DNA sequence represents a plasmid that was used in the exemplification of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACCCCAACTCCTTATCGGAACA 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                    Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                         Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITICATGITIGCCAACAAGCACCITIATATACTCGGTGGCCTCCCCACCACCACTTITIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGTCGCGTCCTGTCACGTACGAATCACATTATCGGACCGGACGAGTGTTGTCTTATCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATGATGATAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITICATGITIGCCAACAAGCACCTITIAIACTCGGIGGCCTCCCCACCACCATTITI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gradactartitacataaatagictacaccetigiataccciccaatacactaccacac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.9%; Score 546.4; DB 12; Length 5038; 99.8%; Pred. No. 1.7e-166; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5038 BP; 1342 A; 1178 C; 1198 G; 1320 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                         Frimpong K,
                                                                                                                                                                                                                                                                                         Madden K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 18; Page 395-403; 555pp; English
                                                                                                                                                                                                                                                                                         Harwood S,
2002US-0396335P.
2002US-0398617P.
2002US-0427231P.
2003US-0456496P.
                                                                                 03-JUN-2003; 2003US-0474940P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    al Similarity 99.8
547; Conservative
                                                                                                                         INVITROGEN CORP.
                                                                                                                                                                                                                                                                                       Bennett RP, Welch PJ,
                                                                                                                                          BENNETT R P.
WELCH P J.
HARWOOD S.
                                                                                                                                                                                                      MADDEN K.
FRIMPONG K.
FRANKE K E.
                                                                                                                                                                                                                                                                                                                                WPI; 2004-132944/13
18-JUL-2002;
26-JUL-2002;
19-NOV-2002;
24-MAR-2003;
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(FRIM/)
                                                                                                                                          (BENN/)
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  BARRAR BA
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AAT13636-731 show open reading frames 13, 20, 22-30, 32, 38, 41-46, 50-60, 62-63, 66, 68-79, 81-87, 91-92, 96-98, 101-103, 106-127, 129-130, 140 -146, 148-150, 152 and 154 from a total of 154 ORFs identified in the Autographa californica nuclear polyhedrosis virus (AcNPV) clone 6. Each gene is numbered according to its position in the virus genome beginning at the left end of the linear map, and irrespective of its crientation.

The direction of transcription is relative to that of the polyhedrin can of the 154 ORFs identified it was found that some of the ORFs (ORFs 27, 30, 32, 71, 86, 123, 126 and 127) are dispensable for virus replication in cell culture or insect larvae. These genes can be deleted from the genome to: (a) provide additional sites for inserting single or multiple copies of foreign genes; and (b) to reduce the size of the virus complementary strand relative to the polyhedrin gene. The present sequence is designated ORF 152, and is on the complementary strand relative to the polyhedrin gene. (Updated on 16-OCT-2003 to standardise
                                   480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Autographa californica nuclear polyhedrosis virus clone 6; disruption; non-essential gene; heterologous protein production; expression vector; baculovirus; ss.
                                                                                                                                                                                                                                                            481 GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAG
421 GGACGCGCTCCATATCAGCCGCGCTTATCTCATGCACGTGACCGGACACGAGGGGCCCC
                                                                                                                                                        GTCCCGCTTATCGCGCCCTATAAATACAGCCCGCAACGATCTGGTAAAACACACAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence - useful in the prodn. of vectors for enhanced hererologous protein expression, such as interleukin(s), interferon(s) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /number= ORF 152
/note= "corresponds to AcNPV nucleotides complement
(132387-132109)"
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Best Local Sim
Matches 126;
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                                                                                               172
                                                                                                                                               232 (
                                                                                                                                                                                                                                                          ADC51646;
 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The complete nucleotide sequence of the genome of clone 6 of the baculovirus Autographa californica nuclear polyhedrosis virus (AcMPV) has been determined. The sequence is taken from the Genbank record L22858. The patent specification claims a polynucleotide selected from open fee, 68-79, 91-87, 91-82, 96-89, 101-103, 106-126, 129-130, 140-146, 148-150, 15.2 and 154 from a total of 154 ORFs identified by the patentees: See T13636-731. Expression vectors contg. the complete genomic sequence of AcMPV, with the exception that at least one non-essential ORF is disrupted or replaced are useful for the synthesis of heterologous proteins. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                         CTACGTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 231
                                                                                                                                                                                                                                                                                                                                                                                 Autographa californica nuclear polyhedrosis virus clone 6; disruption; non-essential gene; heterologous protein production; expression vector; baculovirus; ss.
                                                                                                                    276 AATTITITIGCAATGCAAAAAGTTCACTTTTGCCTGACACTCCATATACAGTACAATCT
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Autographa californica nuclear polyhedrosis virus complete genome sequence - useful in the prodn. of vectors for enhanced heterologous protein expression, such as interleukin(s), interferon(s) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 133894 BP; 39195 A; 27151 C; 27347 G; 40201 T; 0 U; 0 Other;
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0
                                                DB 2; Length 279;
                                                                                                                                                                                                        CTACTACACTATCAACTTTTTTGCATTACAAAAAAGTTCATTTTTGC 110
                                                                                                                                                                                            CTACCACACATTGAACCTTTTTGCAGTGCAAAAAAGTACGTGTCGGC 278
                                             Score 101.4; DB 2; Length
Pred. No. 2.5e-22;
0; Mismatches 41; Indels
                      BP; 88 A; 36 C; 68 G; 87 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Autographa californica nucleopolyhedrovirus; clone 6.
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                                                                                                                                                                                                                                                                    AAT13635/c
ID AAT13635 standard; DNA; 133894
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                                            tch 18.0%;
al Similarity 75.4%;
126; Conservative (
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                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                  ACNPV genomic DNA clone 6.
                                                                                                                                                                                                                                                                                                                                (revised)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1996-087670/09.
                      Sequence 279
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03-SEP-1996
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OS field)
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                                               Query Match
Best Local
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132324 CTACAAATCGTAGACTATTTTATTAGAATAGTCTACACTGTACGATACCCTCCCAATATA 132265
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                                                                                                                                                                                                                      231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a Bombyx mori (silk worm) polyhedrosis virus in which open reading frame 8 (ORF 8) gene is inactivated. The inactivated orsts gene is useful for suppressing movement of silkworm and efficiently prevents the movement of a silkworm from a chamber in which it is raised. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel Bombyx mori polyhedrosis virus in which open reading frame gene is inactivated, or its variant, useful for suppressing movement of Bombyx
                                                                                                            CTACGTTTCGTAGACTATTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22231 AATTTTTTGCAATACAAAAAGTTCGCCTATGTTTGACATATATACAGTACGAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172 CTACGTTTCGTAGACTATTTTACATAGTCTACACCGTTGTATACGCTCCAAATACA
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Length 133894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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  DB 2;
                                                         41;
                            Pred. No. 4.4e-21;
0; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.6%; Score 93.4; DB 10 ilarity 72.5%; Pred. No. 8.6e-19; Conservative 0; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BmNPV genomic DNA nucleotides 100001-128413
  Score 101.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ds; silkworm; silkworm movement supression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bombyx mori nuclear polyhedrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 5; SEQ ID NO 3; 53pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADC51646 standard; DNA; 28413
  18.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUL-2001; 2001JP-00209305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JUL-2001; 2001JP-00209305
                               75.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (RIKA ) RIKAGAKU KENKYUSHO.
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-516415/49.
                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2003024062-A.
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ABZ10059 standard; DNA; 6289 BP

ABZ10059;

62

61

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The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expressing fusion polypeptides. The invention present DNA sequence represents a recombination region of a plasmid that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                   viral vector, recombination site, recombinant virus, replication-defective particle generation; gene expression inhibition; gene therapy vector; ds, plasmid, recombination region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harwood S, Madden K, Frimpong K, Franke KE;
                                                                                                                                   Viral vector-related plasmid pIB/V5-His-DEST recombination region #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 141 BP; 43 A; 36 C; 27 G; 34 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Pred. .v..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 17; 555pp; English
                                 ADQ48576 standard; DNA; 141 BP
                                                                                                                                                                                                                                                                                                                                                                                         26-JUL-2002; 2002US-039B617P.
19-NOV-2002; 2002US-042723IP.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
                                                                                                                                                                                                                                                                                                                                        18-JUL-2003; 2003WO-US022437
                                                                                                                                                                                                                                                                                                                                                                       18-JUL-2002; 2002US-0396335P.
                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVITROGEN CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BENNETT R P.
WELCH P J.
HARWOOD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MADDEN K.
FRIMPONG K.
FRANKE K E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-132944/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                       WO2004009768-A2
                                                                                                    09-SEP-2004
                                                                                                                                                                                                                                     Jnidentified
                                                                                                                                                                                                                                                                                                      29-JAN-2004
                                                                  ADQ48576;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MADD/)
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RESULT 8
                 ADQ48576
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differentiating between hasentpoolers a method of their regulatory regions in a spociated with at least 1 gene and/or their regulatory regions in a subject. The method comprises concacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG incleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative lymphocytic leukaemia and acute myelogenous leukaemia; as probes for lymphocytic leukaemia and acute myelogenous leukaemia; as probes for chermining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related buy asquences and their complements; and as primers for the related sequences and their complements; and as primers for the sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between complement and/or monitoring of haematopoietic cell proliferation of pateints highly specific classification of maematopoietic cell proliferation of pateints
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pelet C;
                                                                                                          Haematopoietic cell proliferation disorder related DNA sequence #199.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Howe A, Mueller J;
G, Lesche R, Leu E;
Mueller V, Otto T, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.0%; Score 39.6; DB 8; Length 6289; 53.2%; Pred. No. 0.14; ve 0; Mismatches 74; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes a method for detecting and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P, Grabs (
Model F, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 28; SEQ ID NO 199; 117pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berlin K, Braun A, Distler J,
Olek A, Piepenbrock C, Adorjan
Lewin A, Lipscher E, Maier S,
Schwope I, Ziebarth H;
                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002; 2002WO-EP003401.
                                                                                                                                                                                                                                                                                                                                                                                                                                  26-MAR-2001; 2001US-0278333P.
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                                                                (first entry)
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nes 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS
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                                                                                                                                                                                                                                                                                               WO200277272-A2
                                                                                                                                                                                                                                                    Homo sapiens
                                                                16-JAN-2003
                                                                                                                                                                                                                                                                                                                                          03-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Berlin K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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CTTATCGCGCCTATAAATACAGCCCGCAACGCTCTGGTAAAACACACAGTTGAACAGCATCTG 487 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAACAGCATCTG

547 TT 548

62; Conservative

Matches

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4896 AATTTATATAAACAAAAAAACTATTATAAATCCACTACCAAATATCATTCAAAAA 4837
                                                                                                                                                                                                 4836 TAATAATTTTTAAAACATTATTATAAAAAATGGTCACAATTCTTTTTACTCAAAAAATA 4777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fragments of chemically modified genes associated with tumor suppressor genes and oncogenes, useful in designing primers and probes for analyzing diseases associated with cytosine methylation state e.g. cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and oncogenes. Note: The sequence data for this patent did not form part of the printed specification, but know obtained in electronic format directly from WIPO at the bulblished_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
cytosine methylation; ds.
                                                                                                                         172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tumour suppressor gene derived chemically modified sequence #223.
                                                                                                                                                                                                                                                                                                                                                       4776 ATACAACTTTCCTCCCCTATAAAAACGAAAAAAAAA 4739
                                                                                                                                                                                                                                                                          232 CTACCACACTTGAACCTTTTGCAGTGCAAAAAAGTA 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000DE-01019058.
2000DE-01019173.
2000DE-01032529.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (EPIG-) EPIGENOMICS AG
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                                                                                                                                                1896 ААТТТАТТТАТАТАБАССАААТААААСТАТТАТААТСССАСТАССАААТАТСАТТСААААА 1837
                                                                                                                                                                                                                             7836 TAATAATTTTTAAAACATTATTATAAAAATCGTCACAATTCTTTTACTCAAAAAATA 7777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least one spee and/or their regulatory regions in a subject by contacting at least uncleic acid in a biological sample obtained from the subject with at least one reagent or series of reagents that distinguish between methylated and non-methylated CpG dinucleotides within the target nucleic acid. The genes and/or their regulatory regions are preferably selected from MRNL, CSMX2B, EGR4, AR, CDK4, RB2, CDC25A, GPIb beta, MYOD1, CDH3, MYCL1, ELK1, ABL1, APC, BCL2, CDH1, CDKN1A, CDKN1B, CDKN2B, FOS, GSTP1, HIC-1, MGMT, MLH1, MOS, MYC, PTEN, RBL2, TGFBR2, TPT3, CDKN1C, GSK3beta, ESR1, APPR1, BAK1, BAX or HOXAS, Oligomers, peptide nucleic acid (PNA)-oligomers and/or isolated nucleic acids based on the sequences of the genes are useful for detecting the methylation state of all the
                                                                                                              172 CTACGTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting and differentiating between lymphoid cell proliferative
disorders comprises contacting a target nucleic acid with at least on
reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ds; lymphoid cell proliferative disorder; methylation; methylated CpG dinucleotide; single nucleotide polymorphism; SNP; diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphocytic leukemia; small lymphocytic lymphocytic selvemia; small lymphocytic lymphoma; follicular lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nimmrich I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human lymphoid cell proliferative disorder gene derived DNA #57.
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Sequence 9289 BP; 2515 A; 206 C; 2097 G; 4471 T; 0 U; 0 Other;
                                    Length 9289;
                                                                        Indels
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                                                                                                                                                                                                                                                                                                          7776 ATACAACTITCCTCTCCCTATAAAAACGAAAAAAAA 7739
                                                                        74;
                                    DB 4;
                                                                                                                                                                                                                                                                   232 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTA
                                  Score 39.6; DB Pred. No. 0.16;
                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 26; SEQ ID NO 117; 448pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                        ADE84121 standard; DNA; 9289 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-NOV-2002; 2002WO-EP013265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-NOV-2001; 2001DE-01057491.
28-DEC-2001; 2001DE-01064501.
                                  7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2004 (first entry)
                                                                        84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-457621/43.
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                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dinucleotides.
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                                  Query Match
                                                        Local
                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
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us-09-896-888a-1.rng

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CpG dinucleotides within one or more the sequences, or their complements, for determining the cytosine methylation state and or single nucleotide polymorphisms (SNPs), and for differentiating at least two of the medical conditions such as diffuse large B-cell lymphoma, mantle cell lymphoma, chronic lymphocytic leukemia, small lymphoma, mantle cell lymphoma ilymphoma. They are also useful for detecting of a predisposition to, differentiation between subclasses, diagnosis, prognosis, treating and/or monitoring of lymphoid cell proliferative disorder. This sequence
                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                        Score 39.6; DB 10; Length 9289; Pred. No. 0.16; O; Mismatches 74; Indels 0;
                                                                                                                                                                                                                               Sequence 9289 BP; 2515 A; 206 C; 2097 G; 4471 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                 74; Indels
                                                                                                                                                                                                                                                                      7.0%;
                                                                                                                                                                                                                                                                                                                 84; Conservative
                                                                                                                                                                                            above mentioned genes.
                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                          Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                 Matches
    888888888888888
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7896 ААТТТАТТТАТАТАТАССАААТААААСТАТТАТАТАТСАСТАССАААТАТСАТТСАААА 7837 7336 TAATAATTTTTAAAACATTATTATAAAAATCGTCACAATTCTTTTTACTCAAAAAATA 7777 172 CTACGTTCGTAGACTATTTTACATAAATAGTCTACACCGTTGTATACGCTCCAAATACA 7776 ATACAACTTTCCTCCCTATAAAACGAAAAAAAAA 7739 232 CTACCACACTTGAACCTTTTTGCAGTGCAAAAAGTA 269 ઠે Ωp g ò ò

205/c ABZ10205 standard; DNA; 6289 (first entry) 16-JAN-2003 ABZ10205; RESULT 12 ABZ10205/

Haematopoietic cell proliferation disorder related DNA sequence #345. Human; haematopoietic cell proliferation disorder; cytostatic; gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.

Homo sapiens

WO200277272-A2

03-OCT-2002.

26-MAR-2002; 2002WO-EP003401.

26-MAR-2001; 2001US-0278333P.

(EPIG-) EPIGENOMICS AG.

Howe A, Mueller J; G, Lesche R, Leu E; Mueller V, Otto T, Pelet C; Berlin K, Braun A, Distler J, Guetig D, Olek A, Piepenbrock C, Adorjan P, Grabs Lewin A, Lipscher E, Maier S, Model F, Lipscher E, I Ziebarth H; Olek A, Pie Lewin A, Li Schwope I,

WPI; 2003-018942/01.

Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.

Claim 28; SEQ ID NO 345; 117pp; English.

The present invention describes a method for detecting and differentiating between hacmatopoietric cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a

biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the trarget nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells if for differentiating between acute Tymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA caquences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients ö 4896 AATTTATTTATATAACCAAATAAAACTATTATAAATCCACTACCAAATATCATTCAAAAA 4837 Detecting and differentiating between lymphoid cell proliferative disorders comprises contacting a target nucleic acid with at least one 172 CTACGTTTCGTAGACTATTTTACATAAATAGTCTACACGTTGTATACGCTCCAAATACA 0; Gaps ds; lymphoid cell proliferative disorder; methylation; methylated CpG dinucleotide; single nucleotide polymorphism; SNP; diffuse large B-cell lymphoma; mantle cell lymphoma; chronic lymphocytic leukemia; small lymphocytic lymphoma; Human lymphoid cell proliferative disorder gene derived DNA #133. Nimmrich Sequence 6289 BP; 1680 A; 0 C; 1488 G; 3121 T; 0 U; 0 Other; 6.7%; Score 38; DB 8; Length 6289; 52.5%; Pred. No. 0.45; 75; Indels ŝ 232 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTA 269 Maier 0; Mismatches Becker E, follicular lymphoma; diagnosis; prognosis BP. 'n ADE84197 standard; DNA; 9289 Genc 23-NOV-2001; 2001DE-01057491. 28-DEC-2001; 2001DE-01064501. 25-NOV-2002; 2002WO-EP013265 (first entry) 83; Conservative (EPIG-) EPIGENOMICS AG. WPI; 2003-457621/43. Query Match Best Local Similarity WO2003044226-A2 Homo sapiens. 29-JAN-2004 30-MAY-2003 Burger M, RESULT 13 ADE84197/c Matches g g à à ò 원

us-09-896-888a-1.rng

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The invention relates to a method of detecting and differentiating between lymphoid cell proliferative disorders associated with at least cone gene and/or their regulatory regions in a subject by contacting a target nucleic acid in a biological sample obtained from the subject with car least one reagent or series of reagents that distinguish between methylated and non-methylated Sample obtained from the subject with car least one reagent or series of reagents that distinguish between condition. The genes and/or their regulatory regions are preferably selected acid. The genes and/or their regulatory rocesh, GPID beta, MYDDI, CDIN, CDKNIB, CDKNIB, CDKNIB, CDKNIB, CDKNIB, CDKNIB, CDKNIB, CDKNIB, CDKNIC, CGSTDI, HIC-1, MGMT, MIH1, MOS, MYC, PTEN, RBLZ, TGFBRZ, TP73, CDKNIC, CGSTDI, HIC-1, MGMT, MIH1, MOS, MYC, PTEN, RBLZ, TGFBRZ, TP73, CDKNIC, CGSTDI, HIC-1, MGMT, MIH1, MOS, MYC, PTEN, RBLZ, TGFBRZ, TP73, CDKNIC, CGSTDI, HIC-1, MGMT, MIH1, MOS, MYC, PTEN, RBLZ, TGFBRZ, TP73, CDKNIC, CGSTDI, HIC-1, MGMT, MIH1, MOS, MYC, PTEN, RBLZ, TGFBRZ, TP73, CDKNIC, CGSTDI, MGMT, MGMT, MART, BAX C, PTEN, RBLZ, TGFBRZ, TP73, CDKNIC, CGSTDI, MGMT, AMAT, BAX C, MCC, STRIB, SASED ON THE SEQUENCES OF the genes are useful for detecting the methylation state of all the cyclosine methylation state and or single nucleotide polymorphisms (SNPs), and for differentiating manner and polymorphisms (SNPs), and for differentiation manner conditions under such as diffuse large B-cell lymphoma, manthe cell lymphoma, chromic lymphoma, They are also useful for detecting of a predicting of a pretreated genomic DNA derived from the shows manner can of a pretreated genomic DNA derived from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 CTAÇGTTTCGTAGACTATTTTACATAATAGTCTACACCGTTGTATACGCTCCAAATACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
reagent that distinguishes between methylated and non-methylated CpG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.7%; Score 38; DB 10; Length 92
Best Local Similarity 52.5%; Pred. No. 0.54;
Matches 83; Conservative 0; Mismatches 75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232 CTACCACACATTGAACCTTTTTGCAGTGCAAAAAGTA
                                                                   Claim 26; SEQ ID NO 193; 448pp; English
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involved in plant resistance or response to pathogenic infection. Miscomprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a murant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (MI) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            253 WARSSGTWSRSAAKRTYKGYSTSRRAKMMRACRMYSACRRYSRTSYYCGCSYCGSSKWKY 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193 MSKSCSMRMTCSSWCSCCYTCYYGAMCWSCCMSMMYMGSCGCYTRGWKWRSKYSMCCKKY 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 CGCGCCTCCATATCAGCCGCGGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCCGTC 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                  Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 AKYWKYWYKRRGIMSWYGKSYKKKYC--IWWCYMKCMRCYRWRKMMRKKTKYSKRCYCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 CTGCAAAAAACACGCTTTTGCACGCGGGCCCATACATAGTACAAACTCTACGTTTCGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                430 CYGCKWWTYCSYGYMKWYTYMGSYKYSRCYKYMRMYMYKGWMYMMYYSAYSSMMTWYYYY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          364 AGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                       present invention relates to a method (M1) for identifying genes
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                    Zon
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   Hon Y;
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                Zhu T,
   SA,
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 Goff
Glazebrook J, Goff
Whitham S, Xie Z,
                                                                                                                                                                           Claim 27; SEQ ID NO 5263; 899pp; English
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 Cooper B,
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(first entry)
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                  Quan S,
                                                   WPI; 2003-175290/17.
 Chen W,
                                                                                                                                         gene expression
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 Chang H, Ch
Katagiri F,
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29-AUG-2002
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WO200228891-A2 11-APR-2002

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The present invention relates to nucleic acid sequences (ABO67188-ABO71212) from Listeria sp. The sequences are useful as probes and Parimers for identification and/or detection of Listeria (e.g. as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria, and are useful as immunogens in antibisteria vaccines. Note: The sequence data for this patent did not form bart of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                          New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, antibodies and modulators.
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                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; SEQ ID NO 1528; 180pp; French.
                                                                                                                                                                              (INSP ) INST PASTEUR.
(CNRS ) CNRS CENT NAT RECH SCI
                                                                                                                                         04-OCT-2000; 2000FR-00012697.
                                                                                                 04-OCT-2001; 2001WO-FR003061
                                                                                                                                                                                                                                                                                   WPI; 2002-332479/37
                                                                                                                                                                                                                                           Kunst F, Glaser P;
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ö 155 CATACATAGTACAAACTCTACGTTTCGTAGACTATTTTACATAAATAGTCTACACGGTTG 214 258 CAGAACATTCATATAAAGTTACATCCATTGCTCAATTTTTCGGTGCTGTAGAAG 202 215 TATACGCTCCAAATACACTACCACACATTGAACCTTTTTTGCAGTGCAAAAAAGTACG 271 0; Gaps th 6.3%; Score 35.4; DB 6; Length 986; Similarity 56.4%; Pred. No. 1.3; 66; Conservative 0; Mismatches 51; Indels (Query Match Local Best Loc Matches Dp ò

Search completed: October 24, 2005, 18:57:59 Job time : 624.051 secs

Sequence 127, App Sequence 16, App Sequence 16, App Sequence 223, App Sequence 223, App Sequence 315, App Sequence 2311, App Sequence 2311, App Sequence 2411, App Sequence 2411, App Sequence 2414, App Sequence 25, App Sequence 1463, App Sequence 25, App Sequence 25, App Sequence 1463, App Sequence 155, App

Sequence 2215, App Sequence 127, App Sequence 914, App Sequence 580, App Sequence 5148, Ap Sequence 5148, Ap

Sequence Sequence Sequence

Sequence

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Gaps

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1 CATGATGATAAACAATGTAGGGGCTAATGTTGCTTCAACAACAACAATTCTGTTGAACTGTG
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100.0%; Score 564; DB 9; Length 564;
Best Local Similarity 100.0%; Pred. No. 3.3e-175;
Matches 564; Conservative 0; Mismatches 0; Indels
1 US-10-622-088-89
US-09-86-888A-14
US-09-86-888A-14
US-09-86-888A-16
US-09-86-888A-16
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US-09-86-888A-16
US-09-86-888A-16
US-10-173-126-199
US-10-173-126-199
US-10-179-111-89
US-10-18-18-89
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US-09-938-842A-5148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09896888A Patent No. US20020116723A1
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Sequence 126, App
Sequence 60, Appl
Sequence 60, Appl
Sequence 60, Appl
                                                                                                                                                                                October 24, 2005, 20:18:24; Search time 1150.82 Seconds (without alignments) 4044.488 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                564
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
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14: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
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20: /cgn2_6
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                             GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-622-088-126

T US-10-295-074-60

US-10-846-911-60

US-10-939-107-60
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Steven
APPLICANT: Welch, Route
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth E.
TITLE OB INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT PILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-18
PRIOR PILING DATE: 2003-07-26
PRIOR FILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-26
PRIOR PILING DATE: 2002-07-26
PRIOR FILING DATE: 2002-07-19
PRIOR PILING DATE: 2002-07-26
PRIOR PILING DATE: 2002-07-26
PRIOR PILING DATE: 2003-07-3
PRIOR PILING DATE: 200
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Publication No. US20040219516A1
GENERAL INFORMATION:
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LENGTH: 560
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US-10-295-074-60
105-10-295-074-60

Squence 60, Application US/10295074
Publication No. US20330185845A1
GENERAL INFORMATION:
APPLICANT:
TILLE OF INVENT NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: P1013DK00
CURRENT APPLICATION NUMBER: US/10/295,074
CURRENT APPLICATION NUMBER: US/2011-15
NUMBER OF SEQ ID NOS: 60
SOFWARE: Patentin version 3.1
SEQ ID NO 600
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                                                                  Length 560;
                                                                                                                                                          1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCT
                                                                                                              Indels
                                                              Query Match 97.2%; Score 548; DB 21; I Best Local Similarity 100.0%; Pred. No. 6.3e-170; Matches 548; Conservative 0; Mismatches 0;
; OTHER INFORMATION: OPIE2 promoter sequence US-10-622-088-126
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LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
FEATURE:
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ORGANISM: Artificial sequence
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365 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 424
                                                                               481 GTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAACACAGTTGAAAGA
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APPLICANT: NIELSEN, Finn Stausholm
APPLICANT: MIELSEN, Finn Stausholm
APPLICANT: BATT, Tomas

APPLICANT: BATT, Tomas

APPLICANT: BATT, Tomas

APPLICANT: MOURITSEN, Soren

TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS

FILE REFERENCE: 674542-2018

CURRENT APPLICATION NUMBER: US/10/846,911

CURRENT FILING DATE: 2004-05-14

PRIOR PELING DATE: 2000-11-16

PRIOR APPLICATION NUMBER: 60/331,575

PRIOR APPLICATION NUMBER: PA 2001 01702

PRIOR FILING DATE: 2001-11-16

PRIOR PELING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-16
                                                     421 GGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 60, Application US/10846911 Publication No. US20040258660A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: misc_recomb
LOCATION: (561). (566)
OTHER INFORMATION: HindIII site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: Apall site
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OTHER INFORMATION: Aval site FEATURE:
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LOCATION: (629)..(634)
OTHER INFORMATION: Clal site
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LOCATION: (625).. (630)
OTHER INFORMATION: Cla1 site
PEATURE:
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LOCATION: (593)..(598)
OTHER INFORMATION: BamHI
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LOCATION: (573)..(578)
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LOCATION: (586)..(591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                               FEATURE:
NAME/KEY: misc_recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
                                             NAME/KEY: misc recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_recomb
LOCATION: (1156). (1161)
OTHER INFORMATION: Apall site
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LOCATION: (2551).. (2556)
1 THER INFORMATION: ApaLI site
US-10-295-074-60
                                                                                                                                                                                                                                                                NAME/KEY: misc recomb
LOCATION: (625)..(630)
OTHER INFORMATION: Clal site
                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc recomb
LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: Pstl site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
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NAME/KEX: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
OTHER INFORMATION: Aval site
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TYPE: DNA
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100.0%; Pred. No. 1.4e-169;
tive 0; Mismatches 0;
                                                                                                                                              FEATURE:
NAME/CONTINE:
NAME/CONTINE: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
LOCATION: (2128)..(2133)
OTHER INFORMATION: PSEL SITE
FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI SITE
                                                                                                                                                                                                     FEATURE:
NAME/KEY: misc recomb
LOCATION: (2551)..(2556)
CTHER INFORMATION: Apail site
                                                                                    FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 548; Conservative
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APPLICANT: Rasmussen, Peter Birk
TITLE OF INVENTION: Novel Application of Vaccination Against TNF-alpha
FILE REPERBNE: 674542-2020
CURRENT APPLICATION NUMBER: US/10/939,107
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: PCT/DK03/00147
PRIOR FILING DATE: 2003-03-11
PRIOR FILING DATE: 2002-03-11
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.1
SEQ ID NO 60
LENGTH: 2773
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                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: p2ZOp2F expression vector for insect cells
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OTHER INFORMATION: Aval, Smal, and Xmal site
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LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
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NAME/KEY: misc_recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
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LOCATION: (1156)..(1161)
OTHER INFORMATION: Apali site
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; LOCATION: (2551)..(2556)
; OTHER INFORMATION: ApaLI site
US-10-939-107-60
                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: NCOI site
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LOCATION: (625)..(630)
OTHER INFORMATION: Cla1 site
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OTHER INFORMATION: Clal site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: Pstl site
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LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
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LOCATION: (593)..(598
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LOCATION: (2294)..(22
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Ebert, Bjarke Pedersen, Louise Henriette

APPLICANT:

Sequence 60, Application US/10939107
Publication No. US20050180947A1
GENERAL INFORMATION:
APPLICANT: Pedersen, Hans Rudolf

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OTHER INFORMATION: pIB/V5-His-DEST
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WENDER

WENDER

Sequence 89, Application US/10622088

Publication No. US20040219516A1

GENERAL INFORMATION:

APPLICANT: Bennett, Robert P.

APPLICANT: Harwood, Steven

APPLICANT: Frimpony, Kenneth

APPLICANT: Frimpony, Kenneth

APPLICANT: Frimpony, Kenneth

APPLICANT: Frimpony, Kenneth

APPLICANT: Primpony, Kenneth

PRICE REFERENCE: 0942.545007

CURRENT APPLICATION NUMBER: US/10/622,088

CURRENT FILING DATE: 2003-0-18

PRIOR APPLICATION NUMBER: US 60/396,335

PRIOR PELING DATE: 2002-07-18

PRIOR PELING DATE: 2002-07-18

PRIOR PPLICATION NUMBER: US 60/456,496

PRIOR APPLICATION NUMBER: US 60/474,940

PRIOR APPLICATION NUMBER: US 60/474,940

PRIOR PILING DATE: 2003-03-14

PRIOR PILING DATE: 2003-03-18

PRIOR PILING DATE: 2003-03-14

PRIOR PILING DATE: 2003-04-14

PRIOR PILING DATE: 2003-04-14
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                               1 CATGATGATAAACAATGTATGGTGCTAATGTTGCTTCAACAACAATTCTGTTGAACTGTG
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                                                  Gaps
Query Match 96.9%; Score 546.4; DB 21; Length 5038; Best Local Similarity 99.8%; Pred. No. 6.3e-169; Matches 547; Conservative 0; Mismatches 1; Indels 0;
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OTHER INFORMATION: Description of Artificial Sequence:Promoter
OTHER INFORMATION: sequence of the OpMNPV ie2 gene
US-09-896-8894-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application US/0989688A

Patent No. US20020116723A1

GENERAL INFORMATION:

APPLICANT: The University of British Columbia

TITLE OF INVENTION: Insect Expression Vectors

FILE REFRENCE: 80021-44

CURRENT APPLICATION NUMBER: US/09/896,888A

CURRENT FILING DATE: 1908-03-26

PRIOR APPLICATION NUMBER: 60/049,946

PRIOR FILING DATE: 1998-03-26

PRIOR FILING DATE: 1997-03-27

PRIOR FILING DATE: 1997-03-27

NUMBER: OF SEQ ID NOS: 50

SOFTWARE: PATENTIN VET: 2.0
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; LOCATION: (141)...(148)
; OTHER INFORMATION: n may be any nucleotide
US-10-622-088-127
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Publication No. US20040219516A1
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LOCATION: (141)...(142)
OTHER INFORMATION: n is a, c, g,
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APPLICANT: Bennett, Robert P.
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Best Local Similarity 100.0
Matches 62; Conservative
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     NAME/KEY: misc feature
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US-10-622-088-149
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US-10-622-088-149
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                                                          Gaps
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Publication No. US20040219516A1
GENERAL INCORMATION:
APPLICANT: Bennet. Robert P.
APPLICANT: Walch, Peter J.
APPLICANT: Madden, Knuch B.
APPLICANT: Frimpong, Kenneth B.
TILLE OF INVENTION: Viral Vectors Containing Recombination Sites FILE REFERENCE: 0942.545007
CURRENT APPLICATION NUMBER: US/10/622,088
FILE REFERENCE: 0942.545007
CURRENT APPLICATION NUMBER: DCT/US03/22437
PRIOR PLING DATE: 2003-07-18
PRIOR FILING DATE: 2003-07-18
PRIOR PLING DATE: 2003-07-18
PRIOR PLING DATE: 2002-07-18
PRIOR PLING DATE: 2002-07-18
PRIOR PLING DATE: 2002-07-18
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2002-11-19
PRIOR PLING DATE: 2003-10-19
PRIOR PLING DATE: 2003-11-19
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Query Match 81.9%; Score 462; DB 9; Length 462; Best Local Similarity 100.0%; Pred. No. 1.5e-141; Matches 462; Conservative 0; Mismatches 0; Indels
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OTHER INFORMATION: Recombination region of pIB/V5-His-DEST
FEATURE:
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                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.545007
CURRENT APPLICATION NUMBER: 0210/622,088
CURRENT APPLICATION NUMBER: PCT/US03/22437
PRIOR APPLICATION NUMBER: PCT/US03/2437
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR FILING DATE: 2002-07-18
PRIOR PLING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: US 60/396,17
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR FILING DATE: 2003-01-19
PRIOR FILING DATE: 2003-01-19
PRIOR FILING DATE: 2003-01-19
PRIOR FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 165
SOFTWARE: PATENTIN VERSION 3.2
LENGTH: 325
LENGTH: 325
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  Length 147;
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                                                       Indels
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Query Match
11.0%; Score 62; DB 21; L
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 62; Conservative 0; Mismatches 0;
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APPLICANT: OLEK, Christian
APPLICANT: OLEK, Christian
APPLICANT: DISPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
TITLE OF INVENTION: Unmor suppressor genes and oncogenes
FILE REFERENCE: 5013.1005
CURRENT PILING DATE: 2003-01-21
PRIOR APPLICATION NUMBER: DE 10013847.0
PRIOR FLING DATE: 2000-03-15
PRIOR FLING DATE: 2000-03-15
PRIOR FLING DATE: 2000-04-06
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 223, Application US/10221714A Publication No. US20040048254A1 GENERAL INFORMATION:
                                                                                                                                                                          Sequence 199, Application US/10473126
Publication No. US20040234973A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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172 CTACGTTTCGTAG 184
                                               76 CTACAAATCGTAG 88
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SEQ ID NO 223
LENGTH: 9289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.1%; Score 57; DB 9; Length 92; 77.5%; Pred. No. 4e-08; tive 0; Mismatches 20; Indels
                                                                                  Sequence 16, Application US/0989688BA
Fatent No. US20020116723A1
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION:
FILE REFERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,88BA
CURRENT FILING DATE: 2001-06-29
FRIOR APPLICATION NUMBER: US/09/048,911
FRIOR APPLICATION NUMBER: 60/049,946
FRIOR APPLICATION NUMBER: 60/049,946
FRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 16
LENGTH: 92
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 69; Conserva
                                                                  US-09-896-888A-16
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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT APPLICATION NOW: 1258
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 199
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SOFTWARE: PatentIn version 3.0
                             SEQ ID NO 1528
LENGTH: 986
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TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
TITLE OF INVENTION: proliferative disorders
FILE REPERENCE:
CURRENT APPLICATION NUMBER: US/10/473,126
CURRENT FILING DATE: 2003-09-26
NUMBER OF SEQ ID NOS: 1258
SEQ ID NO 345
LENGTH: 6289
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                                                                                                                                                                                                                                 7896 ААТТТАТТТАТАТАТАБОСАААТААДАСТАТТАТАДАДТССЕСТАССАДАДТТСЕТТСАДАДА 7837
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; Publication No. US2040018514A1
; GENERAL INFORMATION:
APPLICANT: KUNST, Frederik
APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT APPLICATION NUMBER: PCT/FR 01/03 061
; PRIOR PLILING DATE: 2001-10-04
; PRIOR FILING DATE: 2001-10-04
; PRIOR FILING DATE: 2000-10-04
; RIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-221-714A-223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-473-126-345
                                                                        Score 39.6; DB 19; Length 9289;
Pred. No. 0.22;
0; Mismatches 74; Indels 0;
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Pred. No. 0.61;
0; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-473-126-345/c
; Sequence 345, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
                                                                        Query Match 7.0%;
Best Local Similarity 53.2%;
Matches 84; Conservative (
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ORGANISM: Artificial Sequence
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Best Local Similarity 52.5%;
Matches 83; Conservative
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US-10-398-221-1528/c
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| SEQ ID NO 1528 | LENGTH: 986 | LENGTH: 986 | LENGTH: 986 | PEATURE: DNA ORGANISM: Listeria monocytogenes-4B | PEATURE: DNA ORGANISM: Listeria monocytogenes-4B | CAGANISM: C
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Run on:

Sequence:

Minimum DB Maximum DB

Maximum

Database

44 111 113 114 114 118 118 118 118

Result . 8

Searched:

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PAT 27-AUG-2002
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JP 2001516225-A/1.

unidentified
SM unidentified
unclassified.

E (bases 1 to 564)
S Grigliatti,T.a.A., Theilmann,D.A., Pfeifer,T.A. and Hegedus,D.D.
Insect expression vectors
Insect expression vectors
THE UNIVERSITY OF BRITISH COLUMBIA
OS Multicapsid nucleopolyhedrovirus
PN JP 2001516225-A/1
PD 25-SEP-2001
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Human DNA
Homo sapi
Homo sapi
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Drosophil
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Homo sapi
Drosophil
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Homo sapi
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Oryza sat
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AK107045 Oryza sat
AC149421 Phakopsor
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15 Homo sapi
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                    CQ610736 S
CQ597683 S
AE012382 N
AC019883 I
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AC005554 I
AC109444 H
AC092187 I
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AL732414
AC142496
AC142497
AK104298
AK070153
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AY070687
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PD 72-001516225-A/1
PD 25-SEP-2001
PF 26-MAR-1998 JP 1998541010
PF 27-MAR-1997 US 60/049946,28-JAN-1998 CA
PHOMAS A GRIGLATHI, DAVE A THELLMANN, THOMAS
A PREIPER, DMAYNE D
PT HEGEDUS
PC CI2NIS/08,C12NIS/06,C12NIS/09/C12N9/22
CC Insect expression vectors
FT Source Location/Qualifiers
FT Source / Organism='Multicapsid nucleof
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100.0%; Pred. No. 6.2e-41;
live 0; Mismatches 0;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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AK104298
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BD070856
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Best Local Similarity
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                                                              RESULT 1
BD070856
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
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TITLE
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CR561569 Danio rer
AP003376 Oryza sat
AC134682 Rattus no
AC035655 Rattus no
AP005031 Streptomy
BD221352 Huma gen
AY327402 Choriston
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S64501 p8.9=8.9 kd
AX766573 Sequence
M83827 Orgyia pseu
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AF512031 Choriston
AE016781 Pseudomon
                                                                                                                                             October 24, 2005, 18:40:53 ; Search time 1072.29 Seconds (without alignments) 7998.346 Million cell updates/sec
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                        GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                        4708233 seqs, 24227607955 residues
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177
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AC134482
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AP005031
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linear VRL 02-AUG-1993
                                                                                                                                      Klysner,S., Nielsen,F.S., Bratt,T., Voldborg,B. and Mouritsen,S. Novel immunogenic mimetics of multimer proteins Patent: WO 03042244-A 60 22-MAY-2003; Pharmexa A/S (DK); Klysner, Steen (DK); Nielsen, Finn Stausholm (DK); Bratt, Tomas (DK); Voldborg, Bjorn (DK); Mouritsen, Soren (DK)
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Orgyia pseudotsugata nuclear polyhedrosis virus transcriptional
trans-activator (IE-2) gene, complete cds; ORF, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                    /note="p2ZOp2F expression vector for insect cells"
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                                                                                                                                                                                                                                                                                                                           /organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
                                                                                            other sequences; artificial sequences.
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/note="HindIII site"
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2128. .2133
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/note="AvaI, SmaI,
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/note="EcoRI site"
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/note="BamHI site"
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/note="ApaLI site"
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/note="Aval site"
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/note="ClaI site"
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'note="ClaI site"
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| db_xref="G1:404519"
| translation="WINWOW;IRMAKQQQVRVARQHRAAKLGRLYKAKKLRAELCEKLQ
LQRVNNDAALAKAFEEEFVYPHFSFYLYILN"
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                                                411 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 470
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                      TATCGGAACAGGACGCCCCCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACA 120
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Wh.X., Stewart, S. and Theilmann, D.A.
Wh.X., Stewart, S. and Theilmann, D.A.
Who, Stewart, S. and Theilmann, D.A.
Characterization of an early gene coding for a highly basic 8.9K
protein from the Orgyia pseudotsugata multicapsid nuclear
polyhedrosis virus
J. Gen. Virol. 74 (Pt 8), 1591-1598 (1993)
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                                                                                                                  121 CGAGGCGCCCGCTTATCGCGCCTATAAATACAGCCGCAACGATCTGGTAAA 177
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/gene="p8.9"
/note="8.9 kda basic protein"
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/db_xref="taxon:164623"
763_.990
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1 (bases 1 to 131995)
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NYNSNFVTSTECNHAVCFKCYVSI VLGKESSYKCSI CNRTTI SCRAYNRDGYVELSTINS
NYNSNFVTSTECNHAVCFKCYVSI VLGKESSYKCSI CNRTTI SCRAYNRDGYVELSTINS
LILRQQLIDVKEAELAHESNARHKLIQELQAELARIRAATARAHIDVNNARSDSQ
LILRQQLIDVKEAELAHESNARLKLIQKQNETLSANNLSLQHQLNTQVI ESRVKMEQFKRQ
HDEFMEKFKLSLS."
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PNSVVSCKFI KKTGDRTPACLQFMLALKTIQDRYMATEEEARTEPSFVI KNLQAQLDA
AQKEARDLQESMERQKQAHNVAWNSSCEQVTALQTTLADMQAQLDRSEALSSTLAEHN
RAANVQI DELRRA VQEKLEAAQSAVVENPERDNARQNTNLHERFRS YVYSTVSDWMI
EDSI KSLQSHVFGAACLPCSVNVEINPPRDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tränslation="mSRSNNANAPTPSNRRRNLSLVRGRRLTYSPPDAASAQRASPPR
SAPRAAPRRVHAVGDPGAPLRASYALPNGVYNLHGDAHFNPPEEDDDILFVDTAAEQA
RQRAVNLHEAVNRHERLRRELGERWTRSPTLLNYSPSYSPTSRSRSPDLIMPEDLQP
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                                                                                                                                                                                                   2 (bases 1 to 4170)
Thellmann, D.A. and Stewart, S.
Tandemly repeated sequence at the 3' end of the IE-2 gene of the baculovirus Orgyia pseudotsugata multicapsid nuclear polyhedrosis virus is an enhancer element
Virology 187 (1), 97-106 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                           nuclear polyhedrosis
1 (bases 1 to 4170)
Theilmann, D.A. and Stewart, S.
Molecular analysis of the trans-activating IE-2 gene of Orgyia
pseudotsugata multicapsid nuclear polyhedrosis virus
Virology 187 (1), 84-96 (1992)
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    4170
/organism="Orgyia pseudotsugata single capsid
nuclopolyhedrovirus"

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                                                                                                                                                                                                                                                                                                                                                                                                                                  Original source text: Orgyia pseudotsugata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 177; DB 14;
100.0%; Pred. No. 5.8e-41;
ive 0; Mismatches 0;
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db_xref="GI:332541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
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627, 634
/gene="IE-2"
657, >1908
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/gene="IE-2"
2017. .2759
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/gene="IE-2"
2915. .2922
/gene="IE-2"
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2984. .3907
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/gene="IE-2"
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gene="IE-2"
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|gene="IE-2"
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/gene="IE-2"
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Best Local Similarity 100.
Matches 177; Conservative
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REFERENCE
AUTHORȘ
TITLE
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MEDLINE
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AUTHORS
TITLE
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polyhedrosis virus (AcMNFV) deposited in GenBank Accession
Number L22858"
                                                                                                                                                                                                                                                                                                                                              OPU75930 131995 bp DNA circular VRL 25-MAR-2003
Orgyia pseudotsugata multicapsid nucleopolyhedrovirus, complete
genome.
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GALDNALVVNJUKOLCDALNDLHANTGYIHNDVKLENVLYFGARDRYYLCDVGLGKRE
HSPVHDGTLEYFSPEKIRRHNYARSPDWYAVGVLAYKLLTGGRHPFERSADEVLDLAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ahrens, C.H., Russell, R.L., Funk, C.J., Evans, J.T., Harwood, S.H. and Rohrmann, G.F.
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                                                                                                                                                                 CGAGGCCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 656
                                                                                                                                 CGAGGCCCCGTCCCGCTTATCGCCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                            540 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTATCTCATGCGCGTGACCGGACA
TATCGGAACAGGACGCGCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA
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Submitted (23-OCT-1996) Oregon State University, Agricultural
Chemistry, Corvallis, OR 97331-7301, USA
'Dase 1 to 131995)
Rohrmann, G.F.
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Submitted (06-MAR-1998) Oregon State University, Agricultural
Chemistry, Corvallis, OR 97331-7301, USA
Sequence update by submitter
4 (bases 1 to 131995)
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Orgyia pseudotsugata multicapsid nucleopolyhedrovirus
Orgyia pseudotsugata multicapsid nucleopolyhedrovirus
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;

    .131995
/organism="Orgyia pseudotsugata multicapsid
nucleopolyhedrovirus"

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/note="ORF1; pk-1; similar to ACMNPV ORF10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence of the Orgyia pseud polyhedrosis virus genome Virology 229 (2), 381-399 (1997) 97271300
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9

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CDS

CDS

CDS

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KTLNNNSDKFTSAHKSFKLEVGARFREQFEQBLQTLDTKLNALDCAAPTRTAPGVVFNR
DVTKHPHLAVFWGRYEDRGYTQIAFARGQEBHFRKRKLEFEEGMDVDVRGRAPPLLA
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SFADCVRRAVHMYIGDAREDLVLRYWPDVDRDVFCNANKQIRAPFSYNYKGGDYSRCL
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APGYGLAENFERRRAVARHPLHYPTFGAALJTRRGGALSERLLLNBFELLARRSDELL
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PLERRINESVDGAVVVPATOTNSI HAFELÇMLLDTFANLINYYVLMKVDDAVAAS
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DLTNTARYYDGAQMVKMGLLYKKIRVPGRAVPDDDIVAEFIETVDEFFRRCPTMLVAV
HWTHGLNRSGYLVCRYMVERLGVSPTDAIARFETARGHKIERTNYLODLLARKHVRGO
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VYGRFCAIGREHFAHHKTACMHILFQFMRNDLTPADERHPCFGVIKDFGRQCKDTYTD
LRTHADALYIHGTTDRQKNALFDLLCCVNASDIDADCYDCVVNKFYATQNKKYKM"
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PIRHALGLPVGDHIHVYCEAAPTCAALPNAMPALYDYMVRRIGEGKRVLVHCYAGASR
SAALAVYYLMRSRQMPYQDALNAVQSKRRVAINDHFVRFLATRCSYRFVNDELKPQIV
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NCHNVTVIKPQLLDYAVQDECGRVEQIDADMSAQQYKKLVASSGVFRKRGVVADETTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIDRHAPLARRVGRRANIFALDAIADIPSDVTNNLQGIIGRFMHFPRCSGLARVADVF
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protein id="AAC59013.1"
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/note="ORF13; lef-1; similar to AcMNPV ORF14"
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                                                                                                                        to ACMNPV ORF1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               6819. .7814
/note="ORF11; similar to AcMNPV ORF11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(8180...9142)
/note="ORF12; similar to AcMNPV ORF13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="ORF15; similar to AcMNPV ORF16"
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100.0%; Pred. No. 5.2e-41;
iive 0; Mismatches 0;
                                                                                                                           /note="ORF10; ptp-1; similar
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQQLQQRIKACSAGCLAGGTPPTSK"
9893. .11362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="unknown"
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                                                                                                .6791)
                                                                                                complement (6129.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
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Best Local Similarity 100.0
Matches 177; Conservative
                                                                                                CDS
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KHLDPLDHYMVAEDPPLGPGKNQKLTLFKEIRNVKPDTMKLIVNWSGKEFLRETWTRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="protein tyrosine phosphatase 2"
protein id="AAC59008.1"
/db xref="d1:1911255"
/translation="MYEASQIDEHVFVGGYYGDNEAMLRFIENHAIASVISLIDSDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAC59004.1"
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SDEFVYVPGKERAVPDTRFKPPVPPKPEHLKSRPSSVATNAAGATPVAPPPPPPSAD
VTTSMPPPPPFPSADVTTSMPPPPPMVDLATSMPPPPPPPPPPPPMVDLATSMPPPINNA
                                                                                                                                                                                                                                                           INNLLIDAMVAETNKNAGDNRSALLDOIKQGKTLKKTQPADGAPATDPRSTLLSEIRQ
GKTLKKLRKIEDQSSTQTLLKDVDTTDKTKTILKNFVTNIDRISKQEQEEKDRLDTIT
KRRPAVEHTDGNSTGNNSDDWRDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VEDS FPIVNDQEVMDVFLVVNMRPTRPNRCYKFLAQHALRWDCDYVPHEVIRIVEPSY
VGMNNEYRISLAKKGGGCPIMNIHAEYTNSFESFVNRVIWENFYKPIVYIGTDSSEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tränslation="MRKNNGASQYPEHLTTVHKRHRLQLSCVWCDDQRSWDPHSAKGL
MFEHMFCCLRIYVQQKIKH"
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'translation="MPGARFVRFSLRLTQEFKENVVAHVDHLMGLRALIDGKVTSADV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRFGFLSRNVLVSACMAVNVQVYAPDATIDMRHQPTIYFRVCQNCHAMADVPAPDDHS
IARYLLAECGAVLVIDHPLDVFGETEEGVNELLEVQRINAGGDL"
                                                                                            RAVRLNRQAVLDLLKLAEDIYADTAYMQADQPEASSRHFATLNRMRLLLIGVQDEDAR
RNLNSVLARIEALLRVDVVNDAEVNVLSGDFYEEYSKYISYQQTFAQTPTASASQQTQ
                                                                 /translation="MMERQYQSVRSYLINNQHNAIAAGPFLQRVAGPEAHSVGRNVGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(4125. .4739)
/note="ORF6; lef-2; similar to AcMNPV ORF6"
                                                                                                                                                                                                                                                                                                                                                    complement (2533, .3270)
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/codon_start=1
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/note="ORF8; similar to AcMNPV ORF4"
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/note="ORF7; similar to ACMNPV ORF5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CNRFLEAGDRAPAVIVKAAANGGQHSSLICDKV
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complement (3350. .3541)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (5669. 6151)
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/product="unknown"
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fumiferana multicapsid nucleopolyhedrovirus genomic region encoding
the regulatory genes pkip, p47, lef-12, and gta
Virology 271 (1), 109-121 (2000)
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EDSPPIVNDQEVMDVFLVVNMRPTRPNRCYKFLRQHALRWDCDYVPHEVIRIVEPSYV
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MLIEVSLVFKVKEFAPDAPLFTGPAY"
complement (838. .1449)
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TRMSGMRLLALLAARKEKVPPTRRFPGSKRNVCLEKECADGPOSLTKVLTARNMNPLC
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VTHLLIKABNTYKPSNCAKWKĄVTKLCPKANMCKGLNPICN"
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DLHCLYDLERFVGAHLNKRCDAKAKKNKCAEKAALKRVQISADRHALEAAAAPIDADD
GQWSKLTSAQLDEIAREKDIVDRIYQLQLKQDRLIKMDGLKKQ"
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                                                                                                                  8 (bases 1 to 129609)
Carstens,E.B., Liu,J.J. and Dominy,C.
Identification and molecular characterization of the baculovirus
CfmNPV early genes: ie-1, ie-2 and pe38
Virus Res. 83 (1-2), 13-30 (2002)
                                                                                                                                                                                                                                                                              9 (bases 1 to 129609)
de Jonga, J.G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B.
and Krell, P.J.
Complete Genome of Choristoneura fumiferana Multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 (bases 1 to 129609)
de Jong, J.G., Dominy, C.N., Lauzon, H.A., Arif, B.M., Carstens, E.B.
and Krell, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                            de Jong,J.G., Dominy,C.N., Lauzon,H.A., Arif,B.M., Carstens,E.B. and Krell,P.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of Microbiology, University of Building, Guelph, ON NIG 2W1,
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On May 13, 2004 this sequence version replaced gi:30269978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Choristoneura fumiferana MNPV"
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protein id="AAP29797.1"
/db_xref="G1:30269981"
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/note="ORF3; lef2; Ac6/Op6"
/codon_start=1
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Submitted (11-MAY-2004) Department
Guelph, Chemistry and Microbiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (13-MAY-2002) Department Guelph, Chemistry and Microbiology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
/db_xref="taxon:208973"
/country="Ireland"
complement (1. .735)
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/note="ORF4; Ac5/Op7"
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/codon_start=1
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1. .129609
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Unpublished
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REFERENCE
AUTHORS
TITLE
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JOURNAL
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                                                                                             4 (bases 1 to 129609)

Barrett,J.W., Krell,P.J. and Arif,B.M.
Characterization, sequencing and phylogeny of the ecdysteroid
UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis
Viruses isolated from Choristoneura funiferana
J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA replication
                                                                                                                                                                                                                                                                                                                              circular VRL 27-MAY-2004
                                                                                                                                                           Liu,J.J. and Carstens, E.B. Identification, and sequence analysis of the Choristoneura fumiferana nuclear polyhedrosis virus DNA
                                                                                                                                                                                                                                                                                                                                              Choristoneura fumiferana MNPV polyhedrin, complete genome.
KFS12013 RET77329 S78506 S81690 U10441 U18677 U26676 U26734 U53854
U57401 U59008 U70432 U72240 X65395 S46001
AFS12031.2 GI:47157118
                                                                     TATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
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Identification and molecular characterization of the Choristoneura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu, J.J. and Carstens, E.B.
Identification, molecular cloning, and transcription analysis of
the Choristoneura fumiferana nuclear polyhedrosis virus
spindle-like protein gene
Virology 223 (2), 396-400 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xie,W.D., Arif,B., Dobos,P. and Krell,P.J.
Identification and analysis of a putative origin of DNA r.
in the Choristoneura fumiferana multinucleocapsid nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choristoneura fumiferana MNPV
Choristoneura fumiferana MNPV
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 129609)
Lee,H.Y., Arif,B., Dobos,P. and Krell,P.
Identification of bent DNA and ARS fragments in the Choristoneura fumiferana nuclear polyhedrosis virus
Virus Res. 24 (3), 249-264 (1992)
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Virology 209 (2), 409-419 (1995)
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Pseudomonas purga Ariz440

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

Bacudomonadaceae; Pseudomonae.

Teadomonadaceae; Pseudomonae.

Seudomonadaceae; Pseudomonae.

Readom, R., Peulsen, I., Weinel, C., Dodson, R., Hilbert, H., Fouts, D., Gall, S., Pop, M., Martins Dos Santos, V., Holmes, M., Matup, R.,

Razzo, M., Lee, K., Kosack, D., Moesti, D., Wedler, H., Lance, I., Lee, P.,

Holtzapple, E., Scanlan, D., Tran, K., Moazzez, A., Utterback, T.,

Razzo, M., Lee, K., Kosack, D., Moesti, D., Wedler, H., Lauber, J.,

Hoheisel, J., Straetz, M., Heim, S., Kiewitz, C., Eisen, J., Timmis, K.,

Duesterhoft, A., Tummler, B. and Fraser, C.

Complete genome sequence and comparative analysis of the

metabolically versatile Pseudomonas putida KT2440

E. (bases I to 300363)

S. (bases I to 300363)

Rasnan, M., Deek, M., Martins Dos Santos, V., Holmes, M., Brinkac, L.,

Razzo, M., Lee, K., Kosack, D., Moesti, D., Madup, R.,

Holtzapple, E., Scanlan, D., Tran, K., Moazzez, A., Utterback, T.,

Razzo, M., Lee, K., Kosack, D., Moesti, D., Wedler, H., Lauber, J.,

Hoheisel, J., Straetz, M., Heim, S., Kiewitz, C., Eisen, J., Timmis, K.,

Duesterhoft, A., Tummler, B. and Fraser, C.

Direct Submission

Medical Center Dr., Rockville, MD 20850, USA

Localion/Qualifiers

Localion/Qualifiers
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VQESDPGRPLLWHLDIGQVFWYLGGFAFLHYRIEFADGTSSRSPVQRFDIVSPAAGDP
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SLRVDASSVDSKRLTFHLERBWLQSEVNRGKRFAFSYEFSRGGAQRRSQVLDLVLQRK
LYLPLDI I PDATQEDGDASYQGVVHPSRLESGAKWR I PABAELGDGASPAPTVNLHWE
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GQDVTHILRPPTEAVTYDEYSDGVIKAYLPKQFLGNLDLGKDFRLTVVSASFDDGETWR
                                                                                                                                                                                     AE016781 300363 bp DNA linear BCT 12-DEC-2002
Pseudomonas putida KT2440 section 8 of 21 of the complete genome.
AE016781 AE015451
AE016781.1 GI:26557025
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CITATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAA 176
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78. .1985
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LCANVOLALAE I DKYAPLEKRYSIGNINIFALDTIADI ENNLDDFOTI I YEGEKDFVD
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complement(5854. .6387)
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CEVVRNGVVPAAGYSVVKETAVKAISGWVDLQRFALTVGKSPDGVIGTVGSNGYQQLE
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GEROVGAHWYPORIDRIEPLYGEBELRELBLSPYGYVADMORALTLDLHNSDDFVVTF
SDSRRVRELGGPFFRELFRGLPDHQRVWSFGSIEHGRNDLMRPESFILRTQRNSPSVAL
APMESDDAADVDGALVGLVAMGPSNGPQNMPGPESTRYLIPDDNGDYSATVLLDKAWVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDSALGDIEGEIAMPDSDVTHILTGYRMGPPALVDMQANYTSFKVROSIALEGGSHLV
MDKTDGLLSLSVHDLLDPLPVTQTVPLSADAQGVSADLREGTDTELDLGGGLPQRQAA
GRFFKEVLSGLGSARQVYPLADFKALSGNPYLAVRHSEVRTHVSKADGKSALVIFAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFDEDNNLQRLNATAGLLEVYPSTYESDKYQFACEGFKIAVDAGAPASDQARAALADF
QPLLSVTFEHDEVRQHWKSHCTLTFTYKPKPTGPLYSRTATFQFDLQTVFTLNAPASP
EESAGCMLLGQVLWPWQAAEVTEVSGLPSDTPSDLREEIYAFVAFLVKQAVLEGLARB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTSKQAISMASVAPATLIVNPLIRVCYFDDTLTLTAGAQTGDLDMSVVDDGEEGRGSV
VAEGOGRRCYTYAGSKUDAWVAYVLDQVRVQNRETSESRSIYVLVRQRRPELVIDVKQ
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IPGSVFILEGHLILPLELSLHPDARRAASPTGLRVATSPSIGG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypochetical protein"
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TRISNLEBEDKPDLAQQVLÍDALQAMMSBRPGRCKAF RELGTVPRAGYETHEYPTGRTIKTQ
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GHASDDGLELLARLLFPELNAFVKKVDSTPLDRVMFGNIDPLRTQLTVKFPTMGTVVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DFIRANESLMATEGOGPOPAAPRGAEDRTIRLOMFLHRRGASTSEVFYAGFOARTGRW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FYSNDTRHQNAEIEVKVHTPDAYKSTDYTFTRTRAAGGGGNSGSTDPEHEDFDLHPET
DDYWLLSYNHOTFYTAEPKYKAKSDNDRDWTSWYRBREPEREYKYSYTGYYRQYN
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                                                                                                                                                                                                                                                                                                                                                             LATVLSKLPLEFFTNVEFEFERAENGDLTATALAGVIAAEKESFVSPYYESYWRGSVD
CRAYIDLITDELSLKDVLKFRVSGDRVSMELVTVHTATADFTRYEEIVATPQSWTWGH
ACVGLWHAEINVEITASWQIQDLQGATLKLEEYKHKIYPKQDGSFKFEGDPYEDQISA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LTAMI PEQVMÄGLSLADGKRLVPFDFQLPDGMAVFASGYGTAGMRIVDRPVTLAPGQR
HTFSVEPPREGLTWSLEALPGTVGDLGRIDPASGEYRAPPAHAMAGKPVRVRIIATDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKTQQFRLYDGKDQLITASAMSVINPQSHDDAGHGSIDGNGLFTAPSPEVIGQEVQTF
IIKAEYKQGEETYHAAARALVISEPVLAMPAFGAYRPQESANGIDLMNAGKGNVSFEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNGSVGNLPAEQSDYPFLLPDDLAQPVDSALLLTSRFLHRAAYATGLAQMLEGGAFEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LGQPLGQIASLGNGRSRFVPDQQAGRRILGVQRLQAGSTAKGYNALVLVNSQPLVSVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            locus tag="PP1886"
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note="identified by Glimmer2; putative"
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locus tag="PP1885"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          table=11
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transl_table=
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transl_table=
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10329. .14201

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160996 TATCAAAACCTGCAACGCCTGCACCTCGCAGCCTATCTGGAGCAGCCCGCGC 160937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LIGPATLATERHRITIUWTGDLPPGEHQLDGVLVTGHLDWGGFGKVLEYTLRAMVIQT
OCDASADVBANPVDLGEWSYNDFTGPGFTTPPAAFQYRLSWCQVDPDPGNETLATIEL
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FQARFQTEPNSSLBTGLAKGALNFTIRYR"
COMPLEMENT (15402. .17897)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QEPYFOLPHDETQRWSLISNPSRQRBEKRVTRYDSHGNVLTRLLPNOVLETNVWYSAB
EGDBHGFYRNLKTRYQPATGHGAATLLOGAPYZAGLTBLGSYLKQPRLLESSETU
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DDERALQTVEKLVGVDGESKTITLRHALDTGEPLLNLDDNGVEIRYYYDALRRVTREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRTRYRLORAPAROLLLLESTFGYDROGRMASITTTDÄSTGHALATLLEYDEFDREIL
TEDGGPUTVQTLAQDYDEPCCLKSRILKERRKGSDESQATLLRHETYQYDRRGRLQIY
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LLRVETPDGERCRYNYDPENILSGTAPG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                /translation="MMSTSTSVHSNAFNFSSYIESGVDPRTGQYTVSIRLPELQGNDL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                LSESDNRVSEĪILPTANQARMRFTYEDVLĞYLCVRECTTPYGGVERVFYQDAGHKFPS
SAARDKNLPRVTRHEIDPRFGQAAKVVRYEYPGTHNFIGGGSSISWSDDGLDNLYKVP
EDYTYKSIQIQEVRRQSVRTITRTFNRFHLLTEQATAQGDKLLQAFTRYADNAGNFES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAPGKPFEAERNYKYFLCAYDNEQAQQMAYDVKQVETHTLLDGLSRPIFEERADKDSA
TYAGALRPIYRARYDELDQLVEETEIDMLGDGLLELTSHISYDDMGQRYAVLNPDGTT
QVEEIDQVASTDGPVHRAMREVEHSRVSGITETWYNLFEKPVRIERFALDGSTSISLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PVSIKVGNTESAAVILGEQVPDGLERRTVAITGGREOTFEYDPGERQPHWVKAPDGTR
IEYQYRPALGEEPVLRVLSGKEAKYEYDLKNARLTHCEEPGDDENSGYTLDRSHFLSN
GEVKRESRTVDGEAFSMTYDYSFRSRLRAYVDVLGQTQLYDFDDVGRLEKTTLHAPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNDYDGLGRLSREAQGSGAGORVVEYRYDAFDRVREERLADRVNTVYRTYAGHSRNDL
                                                                                                                                                                                                                                                                                                                                                                                                                     RLHLSYLPFGQGHMRLSEVQDESDVLLRLQRSDNSRVELLCYPSGGDDGGPLARYAMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 TATOGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCCTGACCGGACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                          10329. T.14201
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/note="identified by match to TIGR protein family HMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="identified by match to PFAM protein family HMM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /locus tag="pp1888"
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/locus ment(14251..15345)
/locus = "pp1888"
/note="similar to SP:P42185; identified by sequence
similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 300363;
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); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (15402. .17897)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .15345)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.7%; Score 34.8;
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locus_tag="PP1887"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (14251.
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/transl_table=11
                                                                                                                                                                                        table=11
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transl table=
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                                                                                                                               TIGR01643
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Best Local Similarity
Matches 69; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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                              CDS
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SOURCE ORGANISM

AUTHORS TITLE JOURNAL

REFERENCE AUTHORS

REFERENCE

TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

DEFINITION

RESULT 8 AC121979

ACCESSION VERSION KEYWORDS

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coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                   The RPCI-24 BAC Library has been constructed by Pieter de Jong and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Likely pseudogene (HMM Sc=33.79 / Sec struct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="Likely pseudogene (HMM Sc=39.91 / Sec struct
                                                                                                                                                                             NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone.
Location/Qualifiers
                                                                                                                                                                                                                                              1. .155274
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8319_ .8498
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1. 165
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178. 287
rpt family="Alu"
288. 309
rpt family="B4"
437. 551
rpt family="B4"
726. 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="tRNA-Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="tRNA-Cys'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="B4"
10110. .10490
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[130]..1302
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/rpt_family="B4"
1010. .1081
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1855. .4982
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/rpt_family="B4"
5788. .5975
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5316. .5565
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1104. .1269
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1876. .4987
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/rpt_family="Alu"
7670. .7741
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8826. qnnn
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788. .936
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5566. .5711
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rpt_family="B2"
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http://genome.wustl.edu
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                                            SOURCE INFORMATION:
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                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (13-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 2, 2002 this sequence version replaced gi:22476161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAPPING INFORMATION: Mapping the was provided by Dr. Wes Warren, Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                             AC121979 155274 bp DNA linear ROD 13-NOV-2003
Mus musculus BAC clone RP24-289L14 from chromosome 9, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (25-AUG. 2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA. 5 (bases 1 to 155274)
MCPherson, J. D and Waterston, R.H. MCPherson, Submission
Submitted (02-NOV-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA. 6 (bases 1 to 155274)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 (bases 1 to 155274)
McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (21-MAY-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 155274)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (195274)
McLellan,M., Cotton,M., Doebber,A. and Schatzkamer,K. The sequence of Mus musculus BAC clone RP24-289L14
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
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                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                 AC121979.3 GI:24476151
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                                                               160936 CAAGGC 160931
                  CGAGGC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wilson, R.
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AUTHORS TITLE JOURNAL

REFERENCE

AUTHORS TITLE JOURNAL

RFERENCE

REFERENCE AUTHORS

JOURNAL

COMMENT

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45478 CCTCACCAGCTCGCACTCTCCTCGGGGGCGCACGGCTCGCCGTGCCCCTGCCCCACCACGC 45537
                                                                                                                                         CR361569 17-0CT-2004 Danio rerio clone CH211-99120, WORKING DRAFT SEQUENCE, 12 unordered
                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (10-077-2004) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@senger.ac.uk
On Oct 11, 2004 this sequence version replaced gi:51592229.
                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 179571)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemistry Dye-terminator; 100% of reads
Consensus quality: 175712 bases at least Q40
Consensus quality: 17532 bases at least Q30
Consensus quality: 176923 bases at least Q20
Insert size: 178471; sum-of-contigs
Insert size: 179905; 5.5% error; agarose-fp
Quality coverage: 7.91x in Q20 bases; sum-of-contigs Quality
coverage: 8.06x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently consists of 12 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "trus of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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of 45661 bp in length
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of 2169 bp in length
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                                                                                                                                                                                        CR361569
CR361569.5 GI:S4035037
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
Danio rerio (zebrafish)
Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: 2C99120
------ Summary Statistics
Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web Site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
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                                                                                                            RESULT 9
CR361569/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                              /note="Likely pseudogene (HMM Sc=33.19 / Sec struct Sc=-10.52)"
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'note="Likely pseudogene (HMM Sc=20.93 / Sec struct
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51.7%; Pred. No. 48;
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16036. 16182
16036. 16182
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2916. .13104
               rpt_family="B2"
1043. .11114
product="tRNA~Ser"
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19415. .19480
/rpt family="B4"
/rpt family="B2"
/-9470. .1940
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8243. .18309
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4294. .14440
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4507, 1450
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1959. 12092
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7819. .18242
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1472. .11624
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2291. .12465
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3112. .13274
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7585. .17934
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8767. .18948
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                                                                                                                                         rpt_family="B2"
1349. .11370
                                                                                             1238. .11348
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Direct Submassion

Direct Submassion

Direct Submassion

Direct Submassion

Submitted (07-MAR-2011) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(B-mail:tesaaki@misa_affrc_go_ip, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

On Jul 17, 2002 this sequence version replaced gi:20975425.

Genes were predicted from the integrated replaced gi:20975425.

Genes were predicted from the integrated results of the following: GENSCANI.0, BLASTN2.0, BLASTX2.0 as well as Splicepredictor

(October 1998 version). The genomic sequence was searched against NCBI NonRedundant Protein database, nr RFP. Protein homologies of the coding regions were searched against KFP. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP2.0. ESTS represent the identified CDNA sequences using BLASTN 2.0 with the corresponding DDBJ accession no. and RGP clone ID.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein name to indicate the homology covering almost the entire length of partial sequence) is classified as an 'hypothetical' protein.

The orientation of the sequence is from Milsrev to -21M13 of the BAC clone. This sequence of OsNaBa0014K08 clone has an overlap with P0481E12 clone (DDBJ: AP003768) at the position 172,063 to 177,263 to 177,263 of 3 end. Detailed information on versamily with an end of the sequence of 3 end of the sequence of subsection of the sequence of Scholays Ap003063 at the position 172,063 to 177,263 of 3 end of betailed information of this sequence of Scholays Ap003063 at the position 172,063 to 177,263 of 3 end of betailed information of this sequence of Scholays Ap003063 at the position 172,063 to 177,263 of 3 end of 3 end of 3 end of 3 end of 2 end of 3 end of 3 
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                                                                                                                                                                                                                                                                                               Sasaki,T., Matsumoto,T., Yamamoto,K., Sakata,K., Baba,T.,
Katayose,Y., Mu,J., Niimura,Y., Cheng,Z., Nagamura,Y.
Antonio,B.A., Kanamori,H., Hosokawa,S., Magukwa,M., Arikawa,K.,
Chiden,Y., Hayashi,M., Okamoto,M., Ando,T., Aoki,H., Arita,K.,
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Yamagata,H., Yamane,H., Yoshiki,S., Yoshihara,R., Yukawa,K.,
Zhong,H., Iwama,H., Endo,T., Ito,H., Hahn,J.H., Kim,H.I., Eun,M.Y.,
                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta, Magnoliophyta, Liliopsida; Poales, Poaceae,
Ehrhartoideae; Oryzeae, Oryza.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The genome sequence and structure of rice chromosome 1 Nature 420 (6913), 312-316 (2002)
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
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                                     AP003376 BA000010
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VERSION
KEYWORDS
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AUTHORS
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LOCUS AP003376 13aponica cultivar-group) genomic DNA, chromosome 1,
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19 154564: contig of 19806 bp in length
15 154664: gap of 100 bp
15 179571: contig of 24907 bp in length.
10 179571.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102356. .111881
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EMWWSFGGGGGEMAGNWALQSGASHRATADALFTOLDEQTATKIMDVLQRGGAVATQS
EMWWSFGGGGEMAGNWALQSGASSHRATADALFT OLDEQTATKIMDVSS
TAADATNGSLLCI RRHRRRQDBSTRAHDDILRMLVRSSRSGALHLCPGA
SAFHI FSRRGWSR FRPMDGAVVVTVGDQLQACNGGLYKSVAGKPAYSNDDLRGNGGDT
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RITATAATWDOAAFVLSVPRRKPTDETQETLRTSAFPSQHVKKSGHLVEAISSSRLLA
LVSAQSAAAYVMLASSECDLAYPDYRAVVKIFNGYRS"
join (39834. . 39907, 40580. .40722, 41299. .41408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /trānslation="mpyvvgTrGsNCSEAIVIRSSLISRQKEEYPKGYGKSELANPPM
AVGPSLDAKSCTFKHICRDYSGERTLCVSVIENRRFAPVSLDVQNKKEMVNVLQCLDI
SIFFPC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(31081. .31242,31391. .31579,31787. .31815,
315903. .31593. 32132. .32306,32410. .32549,32638. .32770,
33508. .33574,34086. .34243,34332. .34405,34496. .34609,
35132. .35437)
/gene="OSJNBa0014K08.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 CAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGCGTGACCGGACACGAGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 GTGACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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/gene="OSJNBa0014K08.7"
                                                                                         .29650)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8; Length 177263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Indels
                                                                                         .29152,29378.
    .28537,28795. .29152,29378.
                                                                                                                                                                              'note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18.3%; Score 32.4; Dilarity 53.1%; Pred. No. 71; Conservative 0; Mismatches
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join(27978. .28537,28795.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oteIn_id="BAC05583.1"
xref="GI:21902034"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148545
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Best Local Similarity
Matches 69; Conserv
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        gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,join(19222. 1926). 19694. 19848,19915. 20022,20628. 20832, 21203. 21300,21397. 21480,21572. 21649,21807. 21899, 21991. 22020,22277. 22441,22872. 22967,23073. 23252, 23347. 224585,23909. 225692,225770. 25421,24094. 24347, 24428. 24585,24909. 25692,25770. 25423)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRAVGSTALNERSŠRSHSILTVHVRGLDVKNGSTSRGCLHLIDLAGSERVERSEATGD
RLKERQHINKSLSALGDVIFGLAQKNAHVPYRNSKLTQVLQSSLGGGAKTLMFVQINP
DIESYBSTISTLKFAERVSGVELGAARSNREGKDIKELLEQVASLKOTIARKDMEIEQ
LQLLKSKSPNSMTDRNGSNLLRQSTSSTGLSSLPVASQQNQQLSVYTLTPLADTGLAG
SVEAEAEDNASDDGCSVGETEYSPAGASETSAERAYVLILFSFISCAKPSCACDTSGE
                                                                                                                                                                                                                                                                                                                                                                                                                            AAIAHLKRCGFYLEKLAKKGRGNSPQRRGGAPRRLRVPTGNEEDDPPPLAPFALPLGR
QWCCCFGPAPPAGAREVRPPRLTWPPRRHPGCPATTPSRHRGLDDPPRHGLAPGGQAB
RRPPPPRPGRPRRAAAIRRLRPPLTINRLYAEPQLSAASAPVPGRPSRSRPPPRRLATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VAGOPNAATREAPAAAVSSARRVVVVSPSLARRRTTRPPPPPPPLLFSPRVFSASPP
FGLIPRMRSLRLRSGRRGESGGDQAGALILSWVDANYRGYLDEQFCQVEDLQDEASP
NFVEEVVTLFFKDSGRLMSNIEQALCMRSFQKVKREHAVLROKLESYFQLCSCTWAEB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKGILADDRLAKKPSRQYSMEKGSATNRAIPDFRSAAAMSDAMRRARRRSPCHARNTR
NGTRRAGARPDPEFSRQPIRVLGGRSLSVDETWVTSPAAAVFLRHGETRAPAFALGTA
GRRRGEDDMSVIR"
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MQVMNRMHEQFRHDLKGLVDAAENYHKVLAENQKLFNEVQELKGNIRVYCRVRPFLPG
QDGKLTAIDYIGENGEILIANPSKQGKEGYRMFKFNKVFGTHSSQAEVFSDIQPLIRS
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SMSSIVECLLALKDNVATQLGGHISNSTAKTPIRRKLELRETDGPVLSVATPGKRYPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQQRSPLLSCQKINEVVQFKHGTYTDLPAAKI SEMLHSNSLDNAPTQSLLRVVNGILD
ESIERKRGEI PHRVVHLLRNVIQEI EHRIGIQADHIRNQNSI I KTREDKYRSKI KALE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      join(8072. .8086,9178. .9387,9474. .9671,12990. .13120,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHHDRMPSRHLRPSRAAAGQIQAREGRIRPWGLRIRRLLPTLPP"
join16072. 18066;9178. 9387,9474. 9671,12990. 13120,
14072. 14144,14960. 15376)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(16191. .16218,17138. .17280)
gene="GSNBa0014K08.3"
join(16191. .16218,17138. .17280)
gene="OSJNBa0014K08.3"
405. .3547,5098. .5199,6055.
gene="OSJNBa0014K08.1"
                                                                                note="hypothetical protein"
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Allen, C. Allen, H. Ablabooks, S., Amin, A. Angulano, D., Anyalabechi, V. Avogaja, A., Ayodeji, M., Baca, E., Baden, H., Balabooks, S., Amin, A. Angulano, D., Anyalabechi, V. Avogaja, A., Ayodeji, M., Baca, E., Baden, H., Baladranale, E., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Balder, C., Carler, S., Char, C., Carler, M., Carer, M., Carrer, A., Carrer, C., Coyle, M., Care, A., D'Gouza, L., Davila, M., Cree, M., Diagon, S., Carrer, C., Ding, Y., Dinh, H., Diaya, K., Daramo, C., Ding, Y., Dinh, H., Diaya, R., Maran, M., Martin, K., Martin, 
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Submitted (15-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
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Rat Genome Sequencing Consortium.
Rattus norvegicus clone CH230-179K4, *** SEQUENCING IN PROGRESS
                                                                                                                            HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
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                                                                                               GI:25007228
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Unpublished
                                                                                                                                                                                              Rattus norvegicus
                                                                                               AC134482.2
                                                                                               VERSION
KEYWORDS
SOURCE
ORGANISM
   DEFINITION
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AUTHORS
TITLE
JOURNAL
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JOURNAL
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AUTHORS
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AUTHORS
                                                                 ACCESSION
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Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23334632.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold', individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* NOTE: This is a "The true order of the pieces

* consists of 2 contigs. The true order of the pieces

* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2737 AACTAGACCCCGCTCCTCATCAGCTCAGTACATTCTCTCTGGGCCTGGACCCCTTCTATC 2678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 AGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 ATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGC 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: Phrap; version 0.990329
Consensus quality: 190050 bases at least Q40
Consensus quality: 194119 bases at least Q30
Consensus quality: 195054 bases at least Q30
Consensus quality: 195054 bases at least Q30
Estimated insert size: 204504; sum-of-contigs estimation
Q30 basis; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 222256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 107899: contig of 107899 bp in length
107900 107999: gap of unknown length
108000 222256: contig of 114257 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Rattus norvegicus"
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18.3%; Score 32.4; DE
Best Local Similarity 53.1%; Pred. No. 71;
Matches 69; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (113301. .114059)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: CH230-179K4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                       COMMENT
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Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:24158508.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.read/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 4 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Consensus quality: 216551 bases at least Q40
Consensus quality: 211776 bases at least Q30
Consensus quality: 215202 bases at least Q20
Estimated insert size: 208321; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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555 248654: gap of unknown length

655 267829: contig of 19175 bp in length

830 267929: gap of unknown length

930 268946: contig of 1017 bp in length

947 269046: gap of unknown length

100 270958: contig of 1912 bp in length.

100 270958: contig of 1912 bp in length.
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-6908"
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Center: Baylor College of Medicine
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Center clone name: CH230-6908
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Direct Submission
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248655
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269047
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                                                                                                                                                                                                                                                                                                                                                                                                                     Marany, Danate, Marzker, M. Lee., Abramazon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooke, S., Amin, M., Aggudan, D., Anyalabechi, V., Aoyogi, A., Ayodeji, M., Baca, E., Baden, H., Balabechi, V., Angudaranke, D., Barbarer, M., Barantenda, B., Baden, H., Braden, J., Burdar, M., Barantenda, B., Barantenda, B., Banathmed, F., Biswalo, K., Blart, J., Blankenburg, K., Blyth, P., Brown, M., Chen, Z., Chu, J., Cheveland, C., Corkell, K., Calderon, E., Corkerll, R., Calderon, E., Corkerll, R., Canderon, M., Carden, C., Corle, R., Chen, Z., Chu, J., Charder, C., Corkerll, R., Canderon, E., Davila, M., L., Davis, R., C., Davy-Carroll, L., De Anda, C., Dederich, D., Denson, S., Derson, C., Ding, Y., Dinh, H., Davya, K., Jangan, A., Eccotto, M., Eugene, C., Evana, C.A., Carter, M., Cabrisi, A., Garner, T., Garza, M., Gabisi, A., Mangun, A., Harnandez, S., Fillys, M., Hawil, C., Hamilton, C., Hamitton, K., Harnandez, S., Fillys, M., Hawes, A., Handerson, M., Hamilton, C., Hamitton, K., Mangun, A., Harnandez, S., Kallys, M., Mandon, B., Underson, W., Harnandez, S., Kallys, M., Mandon, B., Underson, W., Harnandez, S., Kallys, S., Kallys, S., Kallys, M., Mandon, R., Majus, L., Liu, J., Liu, M., Liu, Y., London, P., Lordon, P., Mandon, R., Majus, L., Liu, W., Martin, R., Martinez, E., Mandoum, B., Morgan, M., Morris, S., McLeod, M. P., Morris, S., Morced, M., Martin, R., Martin, R., Mandoum, A., Mandoum, M., Morris, S., McLeod, M. P., Mortin, R., Martin, R., Martin, R., Martin, R., Martin, M., Morris, S., McLeod, M. P., Wall, M., Martin, R., Martin, R.,
                                AC135655 270958 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-6908, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 270958)
                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                               HTG; HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Rat Genome Sequencing Consortium.
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                                                                                     DEFINITION
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AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MTTTADSATITAQDRSQGRLEPVHAMNEATSHEGPKRSLPGRPP
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/product="putative vitamin B12-dependent ribonucleotide
                                                                                                                                                                                     strain: ATCC 31267,
                            /organism="Streptomyces avermitilis MA-4680"
/mol_type="genomic DNA"
/strain="MA-4680"
/db xrain="MA-4680"
/db xref="traxon:227882"
/noTe="This strain is also named as strain: ATCC
NCIMB 12804 or NRRL 8165.~synonym: Streptomyces
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                                                                                                                                                                                                                                                                                                          complement (42. ,2936)
                                                                                                                                                                                                                                                                                                                                                                                  complement (42. .2936)
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/transl_table=
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/transl_table=
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/gene="lexA"
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                                                                                                    105760 AACTAGACCCGCTCCTCATCAGCTCAGTACATTCTCTCTGGGCCTGGACCCCTTCTATC 105819
                                                                                                                                                                                                                                                             105820 GTTAGCCAGAAGTGAGAACAGGCTCAGGTCCCCTTGTCACACTTCTAAGGGAAGGTCAC 105879
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Submitted (29-MRA-2002) Director-General of Biotechnology Center,
Submitted (29-MRA-2002) Director-General of Biotechnology
National Institute of Technology and Evaluation, Biotechnology
Center; 2-49-10 Nishihara, Shibuya-ku, Tokyo 151-0066, Japan
(E-mail:bio@nite.go.jp, URL:http://www.bio.nite.go.jp/,
Tel:81.3-3-481-845,
Fax:81-3-3481-844,
This work was done in collaboration with Haruo Ikeda (*1), Jun
Ishikawa(*2), Akiharu Hanamoto(*3), Chigusa Takahashi(*3), Mayumi
Shinose(*3), Hiroshi Horikawa(*4), Hidekazu Nakazawa (*4), Tomoni
Osonoe(*4), Norihiro Kushida(*4), Hisashi Kikuchi(*4), Tadayoshi
Shiba(*5), Yoshiyuki Sakaki(*6,*7), Masahira Hattori(*1,*7)
and Sacoshi Omura(*1,*3).
Final finishing process and all annotation were done by H. Ikeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ikeda, H., Ishikawa, J., Hanamoto, A., Shinose, M., Kikuchi, H., Shiba, T., Sakaki, Y., Hattori, M. and Omura, S. Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis Nat. Biotechnol. 21 (5), 526-531 (2003)
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*2 National Institute of Infectious Diseases
*3 The Kitasato Institute
*4 National Institute of Technology and Evaluation
*5 School of Science, Kitasato University
*6 Institute of Medical Science, University
*7 RIKEN, Genomic Sciences Center
Pollowing url is also available.
http://avermitils.ls.kitasato-u.ac.jp.
                                44 AGCCGGACGCAACTCCTTATCGGAACAGGACGCCCCTCCATATCAGCCGCGCGTTATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Omura,S., Ikeda,H., Ishikawa,J., Hanamoto,A., Takahashi,C.,
Shinose,M., Takahashi,Y., Horikawa,H., Nakazawa,H., Osonos,T.,
Kushida,N., Director-General of Biotechnology Center, Shiba,T.,
Sakaki,Y., and Hattori,M.
                                                                                                                                                                                     104 ATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptomyces avermitilis genomic DNA, complete genome, section
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Proc. Natl. Acad. Sci. U.S.A. 98 (21), 12215-12220 (2001)
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Streptomyces avermitilis MA-4680
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KEYWORDS
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Tue

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Gaps

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33; Indels

Mismatches

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52; Conservative

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AMILKGRSINYLCLHRILHEGVPQDEEGGIPDQFBAAPTSKIGQDLLRILBUWSDETETGD
RDDLTPGVSDRAMAQVSVSRECLGATKCAYGABCPABMSBRAKLABEVVATNHALLA
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LQGBFTLGEI KNYFAADPFTCLFGILSAMGGYTUGLFSSMRAQUAAEELRSRIPEFPII
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ARQKAVEDAGGNGFMAVAATHAALLMAQGAGRILVRASGDRGVVAVLDGRLATARYGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APSVPARAGATAASADSDGCSDAVDPAAPFAAASTVPSASRVPSAFSVTSAPSVTFAT
APRAPAPEIGUTKALAGRQAVSVTRAADDLIGRVEDWGPTVTPAGTFQLAPVRPERDL
PLLGRWMDPPAVAFFWLLAGDESVTEQLGGDGRSVPCLGVLEGTPMSYWEIYR
ADLOSLARRIYPARPHTGIHLLIGGVADRGRGLGSTLLRAVADLVLDRRPSGRRVVAE
PDLRNTSSVSAFLGAGFRFSAEVDLPDKRAALMVRDRPLRDLL"
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TQAPLAPATQVVFVPEVRTPVVQASESVPPVGRARESERLRGTTADPLDHPEAQTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /trānslation="MAVTKSAVASLKREAEGAHAAHEGILRRQSARESAARTYARALP
IVVRVARGITIEGADGRRYIDCLSGAGTLALGAHHPVULEATRKVLDSGAPLHYLDLA
TVVKDAFTTELRRTLARGALARANQFCGAPGTDAVBAAFKLVRTAGRSGLLAFTGA
YHGMTAGALEASGGATDGRVARLPYPQDYRCPFGIGGERGAELGARWTESLLDDVKSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MPPTDASTDAEPATSADPARIAVSARSAADSEDTLELRLPDELV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DAPQTAPPADAVTVVALLAREAAGSRRAPRPAHSAVDHCAVDHSADLVGRVADSVRRT
AVFIDDRRARPADEPDLFLAAEQALLLGHPLHPTPKSREGLSEAEARLYSPELRGSFA
LHWLAVAPPVLATNSAWTERGRPVPAEQLTARLAGDGLPMPDGFAALPLHPWQIREIR
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RKELHRGVEVHRLLRSGLGEQWQAAHPGFDIVRDPAWLAVDDQHGNAVPGLDVMIRHN
PFAPTDDVSCVAGLVSPRPWPQPTEQPRPVMRSRLAEIIIRLAGRTGRPRGAVATEWF
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RFLADVATGPARLRTPLPTRLLDSPVLRCKANLLTRLHGLDELVGPVDTQSVYVTIAN
PLHS"
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BRGVVPDWVLSKALGGSLPLAVVYRDDLDWOPGRAHGFRGNQLMAAGTATLA
YVREHKLABRAQTLGARMLDQLRSIATBFPCVGEVRGRGLMIGVELVRABEDBRAVSP
GSGDFÄSLDTAGAGPRPAAPELAAAVQRECLRRGLI VELGGRHASVVRLLPPLTI SDB
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DTRASSESSPSASSAGDDKIKIPDDIRDKLKERGIDIDKWKNGAWKNWNRDDWLREAN
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                                                                                                                                                                                                                                                                                                                                                                                                    LKASLPDFWYTTDRNQVRRSLTAIDEAAKKTEVTEVTEVAEVTEEAAKESEGA"
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(protein id="BAC70178.1"
/db_xref="GI:29606115"
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|product="putative secreted protein"
|protein id="BAC70179.1"
|db_xref="GI:29606116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
/transl_table=11
/product="hypothetical_protein"
/protein_id="BAC70176_1"
/db_xref="G1:29606113"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  trans] table 11

product="hypothetical protein"

protein_id="BAC70177.1"

db_xref="G1:29606114"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (8549. .10609)
                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (7376. .8509)
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/transl_table=11
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'note="SAV2468"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="SAV2465"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="SAV2467"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="SAV2466"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon start=1
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128986 CCTCCACCGAACCGGACGCGTCGCCCTTGATGATGAGGTTGAGTTCCTGCACCAGACCGG 129045
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PI JULIE SUDDUTH KLINGER, CHRISTOPH REINHARD, KLAUSE GIESE, FILIPPO PI RANDAZZO,

PI GIULIA C KENNEDY, DAVID POT, ALTAF KASSAM, GEORGE LAMSON, RADOJE PI BRANDAZZO,

PI BRANDAZZO,

PI GIULIA C KENNEDY, DAVID POT, ALTAF KASSAM, GEORGE LAMSON, RADOJE PI BRANDARC, IVAN LABAT,

PI BRANDAUR CRKVENJAKOV, MARK DICKSON SNEZANA DRWANAC, IVAN LABAT,

PI BIRGIT STACHE CRAIN

PC CIZNIS/09, COTXII4/47, COTXII6/18, CIZNII/19, CIZNII/19, CIZNII/21 PC

CIZNIS/00, CIZNIS/00

CC n = A,T,C or G Location/Qualifiers

FT misc_feature (1) (921).
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Williams, L.T., Escobedo, J., Innis, M.A., Garcia, P.D., Klinger, J.S.,
Reinhard, C., Giese, K., Randazzo, F., Kennedy, G.C., Pot, D.,
Kassam, A., Lamson, G., Drmanac, R., Crkvenjakov, R., Dickson, M.,
and Crain, B.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
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RANDAZZO,
GIULIA C KENNEDY, DAVID POT, ALTAF KASSAM, GEORGE LAMSON, RADOJE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76 CGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCCGTCCC 135
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RADOMIR CRKVENJAKOV,MARK DICKSON,SNEZANA DRMANAC,IVAN LABAT,
DENA LESHKOMITZ,DAVID KITA,VERONICA GARCIA,LEE WILLIAM JONES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97 gecercina a necescrite contra cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60/085537 PR
58 CCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTATGTCATGCGCGTTGACCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 GACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 GGCAGCTGCGCNCCAGGTGGCTGTCCCACGCCGGTCTCCGCGCCCTGCCCCGGTGCGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human gene and gene expression product V
Patent: JP 200254055-A 2465 15-OCT-2002;
CHIRON CORP,HYSEQ INC
CHIRON CARP,HYSEQ INC
CHIRON CARP,HYSEQ INC
CHIRON CARP,HYSEQ INC
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Pred. No. 1.1e+02;
0; Mismatches 64; Indels
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/organism="Homo sapiens"
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1. .921
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 921 bp
                                                                                                                                                                                                               118 ACACGAGGCGCCCGTCCCGCTTATC 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BD221352.1 GI:33031122
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ilarity 51.5%;
Conservative (
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Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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Best Local Si
Matches 68,
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BD221352/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
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VERSION
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AUTHORS
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JOURNAL
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SOURCE
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t 12

Query Match Best Local Similarity

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/codon start=1
/product="late expression factor 2"
/product="late expression factor 2"
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/db_xref="GI:3749917"
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                       PLNVMPPPPPPNVPPPPPLDNLLLDAMMSEPRKGATDRSALFDQ1KWGATLKKAQPVE
PSDLRGDNLOJRTGATLARTGRLEDBDLGGFKKGREGILGVLVNTVLGSRRGGIDSE
RSDVATSESTSGASADTRABKSKSELKHAAHLYNFAKDSKLYNIQKVNNSELTKI
LENVGPLLKRSPRTAENVEKANAGLYLFRQHVTLPKNALDAQPAPELYAADPOFYVO
                                                                                                                                                                                                                                                                                                                               /translation="MDNYSYRPTIGRTYVYDNKYYKNLGSVIKNAKRKKHLLEHEEDE
KHLDPLDHYNVABDPFLGPGKNQKLTLFKEIRNVKPDTWKLIVNWGGKEFLRETWTRF
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|/translation="WADSTWITLEYRWSSKTGASLENQADLECLYDLERFVGAHMN
|/translation="WADSTWITLEYRWSSKTGASLENQADLECLYDLERFVGAHMN KQIETSCKKKKQAEERAESAALKRVELAADRWAMQAKAAPYCADDGRWSTLSQQQLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="WASARFIKESLRVTQGFKENIVADITHLARLRALIDGKVTHTDV
HRFGFLDRNALVEACMAVNVQVYPDGTIRLNPKTIYFRVCQKCHAVADVPAPDDHSI
ARYLCAACGMVLVIDHPLDVFGDTEEGVNELIEVQRINAGGDL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MYDANQIDENLFVGGYYGNNEAMLQFIKKHDIESVISLIDSDVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="mnrpmmrtanapulysnhdydregirrdinslrrsvhelctrst
TGFDCNRILELSSSSNDVITKSPVIIKNSAATVGQSALVCDKV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNLSAADIVAETTRPNPTVDWNNATHRLAAKKSKRTISFDSEQDAQOFATRIKQLLNN
NGVNLNTTLKPPVPPKPAHLSRPNFMFVGDKVTGNTPPPPNGTSPQPGVNVPPPPVAP
                                                                                                                                                                                          'note="ORF 1; ph Op3/Ac8; major occlusion body protein"
                                                                                                                                        IEDLLFAGRYDDARAFIQAVDAPEDMKLKKFLTVANQLSTRGQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDRNKEIVDRIYKLQLKQDCLLNNKNAF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1247. .1858)
/note="ORF 3; lef-2 Op6/Ac6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ORF 7; ptp-2 Op9"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAQ91737.1"
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                                                                                                                                                                                                                                                                              /protein_id="AAQ91696.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (1861. .2124)
/note="ORF 4; Op7/Ac5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .4168)
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/note="ORF 6; bro Ac2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (828. 1220)
/note="ORF 2; Op5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2171. .2608
/note="ORF 5; Op8/Ac4"
                                                                                                                                                                                                                       /codon_start=1
/product="polyhedrin"
                                                                                                                                                                     complement (1. .738)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="unknown"
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/product="unknown"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 11500 to 13512)
Barrett,J.W., Krell,P.J. and Arif,B.M.
Characterization, sequencing and phylogeny of the ecdysteroid
UDP-glucosyltransferase gene from two distinct nuclear polyhedrosis
J. Gen. Viruses isolated from Choristoneura funiferana
J. Gen. Virol. 76 (Pt 10), 2447-2456 (1995)
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//bcatein id="AAQ91783.1"
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//translation="wrrcycovyxyldinglocal-provided RTVKLNRATLIDLLKLAENIYADTAYMQVNTIESSRHFATLMRMRNLLLANVQDEHFRN
RTVKLNRATLLDLLKLAENIYADTAYMQVNTIESSRHFATLMRMRNLLLANVQDEHFRN
VASSIVARTRONLANVOVSITVLAGGBYERSKYRTROVYSTDTLPPPPPPLAPPI
PETTQAFVARSPEPPAQAFVARSPPPRAQAFVARSPPPRAGFTSY
FVAPSPQATQTPSPRQTFAAPSPVPAESPQPTRAFPTPEGTLSRGAADEFEYRAGTSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fumiferana multiple nucleopolyhedroviruses share domain homology to eukaryotic primases
Virus Genes 13 (3), 229-237 (1996)
                                                                                                                                                                  circular VRL 08-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Canada
On or before Oct 8, 2003 this sequence version replaced gi:1117788,
gi:2581770, gi:1754838, gi:4092491.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Barrett, J.W., Lauzon, H.A., Mercuri, P.S., Krell, P.J., Sohi, S.S. and
                                                                                                                                                                                                                                                                                                                                        (CEDEFNPV)
                                                                                                                                                                                               Choristoneura fumiferana defective nucleopolyhedrovirus complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (20-JUN-2003) Molecular Virology, Great Lakes Forestry
Centre, 1219 Queen St. E., Sault Ste. Marie, Ontario P6A 2E5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,X., Barrett,J., Pang,A., Klose,R.J., Krell,P.J. and Arif,B.M. Characterization of an overexpressed spindle protein during a baculovirus infection
Virology 268 (1), 56-67 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecular analysis of the p48 gene of Choristoneura fumiferana multicapsid nucleopolyhedroviruses CfMNPV and CfDEFNPV J. Gen. Virol. 80 (Pt 7), 1833-1840 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 80268 to 81693)
X., Lauzon,H.A., Sohi,S.S., Palli,S.R., Retnakaran,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The putative LEF-1 proteins from two distinct Choristoneura
                                                                                                                                                                                                                                                                                                                                     Choristoneura fumiferana defective nucleopolyhedrovirus Choristoneura fumiferana defective nucleopolyhedrovirus
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/organism="Choristoneura fumiferana defective
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                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
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/product="viral_capsid_associated_protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/db_xxef="taxon:74660"
join(12949. . 131158.1. .20)
/note="ORF 149; 1629 capsid Op2/Ac9"
                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                    AY327402 AF068194 U10476 U23422 U78194
                                                                                                                                                                     131158 bp
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                                                                                                                                                                                                                                                                              AY327402.1 GI:37499238
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                          37 TAAGATCGNGCC 26
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                                                                                                           RESULT 15
AY327402/c
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KEYWORDS
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complement (4155. .4676)
/note="ORF 8; ptp-1 Op10/Ac1"
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VQEFSARCPGMLIGYHCTHGLNRTGYLVCRYIIDKLHVSFTDAIARFEBARGHKIERR
NYLEDLLKRHVRR.
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DPTI KLIGWWYNKFCVLTYWYR I IRGYPABLI ITRLQNVYTXI I KREYDSRNNALAMG
DVYGRFCGI GKDHFAQHKMBSVY I FRQYMGSBVTYADIBRFPCFSVI KDFGRQYKETYK
DI QLQVDI LHSHAMTDKQKNALFDLLCCNNASDI DVDCYDY I VKKFYNIAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6450. .6723
/note="4 copies of a 30 bp imperfect palindromic sequence, location similar to Ac hrla"
/function="enhancer, replication origin"
complement(6723. .7811)
/note="ORF 10; Op20/Ac20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y I ESVWRRRHYVPMEALD-SVQFDTNLGTLAGETLKCMSVPLYTEIDLPFFDCTQVCE
DPGASYFFVGEGDTYVVNGHKLAVGSYCTTNSVPRDCNRETSVVLMSLNQWTCIAEDP
RXFAGTSNMTQLAGRQHFDR I LBQSDRNVLFDRLGREVNVATNTFRRSWDELLEDG
TRYFAGTSNMTOLAGRQHFDR I LBQSDRNVLFDRLGREVVNYVTHTSVRPNFETGECDGDGA
VTRVRHVVPGDRSSVCAS I VDGLDTTTASHRRFRVECVNYYTTS GUFSNNKLLCPSDTF
DSNTDAAFAEVVGSY PLSGNGLDEPTHRFFLDTRSR I RXNDVRGL I N"
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/db_xref="G1:37499279"
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SATLAVYYYMKKWQVSYEKALRFVNNKRNVALSDHFVRFLSSRCTYRFVNNKLKIHVG
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PTPVKTLYFESAPLKEQDTADEEEEQQSSFRMLEIISEPRVQFQFPESSSLDRLSSPP
PIVQSSSSPNSPDSGIDYDIPQPFYSVPNKVVCKYLCRTHATLCA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _protein_id="AAQ91675.1"
|db_xref="GI:37499276"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein id="AAQ91663.1"
db_xref="G1:37499264"
translation="MYRILIVLFLFALLYIVVWPFYQAYQHIQTAQHDYNDTLTDRMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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18.1%; Score 32; DB 14; Length 131158;
Best Local Similarity 87.5%; Pred. No. 94;
Matches 35; Conservative 0; Mismatches 5; Indels 0;
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'product="actin rearrangement inducing factor"
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/note="ORF 11; arif Op19/Ac21"
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/note="ORF 12; Op18/Ac19"
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/protein_id="AAQ91753.1"
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/note="ORF 9; Op11/Ac11"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 507)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Hood, L., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                    AQ297217 507 bp DNA linear GSS 15-DEC-1998 HS_2266_A1_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=15 Row=A, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
                     B0720271
B18434062
B18434062
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CG295117
CK193317
CK192985
CC06683018
CO0683018
CC98675
CF886875
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High Throughput Sequencing Center
Whigh Throughput Sequencing Center
William Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3861
Fax: (206) 616-3861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 8;
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|mol_tvpe="genomic DNA"
|db_xref="taxon:5606"
|clone="plate=2266 Col=15 Row=A"
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Pred. No. 5.1;
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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                                                                                                                                                                                                             GGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAG 124
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. Bases 1 to 402)

S. Vazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldaelli, R., Hill, D. P., Bult, C., Hume, D. A., Quackenbush, J., Schridh, I. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Bradt, D., Brusic, V., Chobnia, C., Corbani, L. E., Cousins, S., Dalla, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I. J., Jarvis, E. D., Kanai, A.,
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                                                                                                                                                                                                                                                                            Answering pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 TCGGAACAGGACGCGCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues.
Tissues were provided by Vassilis Aidinis ( Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece ) whose assistance we gratefully
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cNNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-forme Dec
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/clone="L230041A03"
/tissue type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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Mus musculus
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BY077721
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Best Local Similarity 51.7.
Best Local 75; Conservative
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Tue Oct

89 CTTAATGTGATCCCCCCCCCTTTCCTTTCTCCGTAGCCTGACGCGGCAGCAGCGCCGTTT 148

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Matches
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BY338426
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Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V. Lee, Y., Lehhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Percoky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reid, J., Ringy, B.Z., Kingwald, M., Sandelin, A., Schneider, C., Sequile, G.A., Setou, M., Shinada, K., Verardo, R., Wagner, L., Wahlested, C., Wannagiswa, M., Watnabe, Y., Wells, C., Wilming, L.G., Wynhaw-Boris, A., Yanagiswa, M., Yang, I., Yang, L., Yan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Wahi, Y., Kawai, J., Aizawa, K., Srakazume, N., Kaswa, I., Miyazaki, T., Waki, K., Sasaki, D., Shibata, K., Shinadawa, I., Wayazaki, P., Sakai, K., Sasaki, D., Shibata, K., Shinadawa, J., Washilo, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fax: 81-45-503-9212
Fax: 81-45-503-9212
Fax: 81-45-503-9212
Fax: 81-45-503-9212
Alzawa, K., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Tmotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, Y., Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Namm. Genome. 12, 673-677 (2011)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequence din Mouse Genome Encyclopedia: Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Net Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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/clone_lib="RIKEN full-length enriched, adult male liver"
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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Matches 75; Conservative
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Gaps

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3 CTTATCGTGACAGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA 62

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348 bp mRNA linear EST 11-DEC-2002 BY338426 RIKEN full-length enriched, whole joints Mus musculus cDNA clone L230014G21 5', mRNA sequence.
BY338426
                                                                                                                                                                                                                                                                               CV068875 931 bp mRNA linear EST 24-AUG-2004 f2_new_chopped.fasta.Contig488 Preamplified custom cDNA library in pCMVsport6.1 (ResGen, Invitrogen Inc.) Emiliania huxleyi cDNA, mRNA
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Emiliania huxleyi
Eukaryota; Haptophyceae; Isochrysidales; Emiliania.
1 (bases 1 to 93).
Wahlund,T.W., Zhang,X. and Read,B.A.
Expressed Sequence Tag Profiles from Calcifying and Non-Calcifying
Cultures of Emiliania huxleyi
63 TCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                  149 CCTCACCAGCTCGCACTCTCCTCGGGGCCCACGGCTCGCCGTGCCCCTGCCCAGCANGG 208
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 348)
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/clone_lib="Preamplified custom cDNA library in
pCWPsport6:1 (ResGen, Invitrogen Inc.)"
/note="Emiliania huxleyi grown in Artificial Seawater
(Gulllard's F/2 media)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39 ACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCAGCCGCGGTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Micropaleontology (2004) In press
Contact: Betsy Read
Department of Biological Sciences
California State University San Marcos
333 S. Twin Oaks Valley Road, San Marcos, CA 92096-0001, USA
Tel: 760 750 4129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 ATCTCATGCGCGTGACCGGACACGAGCGCCCCTCCCGCTTATCGCGCCT 148
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/organia="Emiliania huxleyi"
/mol_type="mRNA"
/strain="1516"
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Pred. No. 8.2;
0; Mismatches
                                                                                                  123 AGGCGCCCGTCCCGCTTATCGCGCC 147
                                                                                                                             209 GACAGAGCGTCCCGCTTCTCC 233
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Gaps . 0

10, .,

Length 348; Indels

AUTHORS

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Readmalls burnerlas, kodentia; Sciurognathi; muridae; Murinae; Musc. C Razaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quascerbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Brada,D., Brusic,V., Crobani,L.E., Cousins,S., Dalla,B., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Martais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pevran, W.J., Pertea,G., Pescole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Wangor,L., Wahlestedt,C., Sengle,C.A., Setou,M., Shimada,K., Sullana,R., Tawasawa,Y., Taylor,M.S., Taesdala,R.D., Tomita,M., Verardo,R., Wangor,L., Wahlestedt,C., Wang,Y., Watenabe,Y., Wangor,L., Wahlestedt,C., Wang,Y., Watenabe,Y., Wangor,L., Wahlestedt,C., Wang,Y., Watenabe,Y., Hayatsu,N., Hirozane-Kishikawa,T., Yang,Y., Zimmer,A., Yang,I., Yang,L., Yang,L., Makawa,T., Rawai,J., Aizawa,K., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Anglanda, K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Anglanda, A., Najarishizaki,Y., Rogers, C., Barande, M., Waterston,R., Lander,E.S., Anglanda, K., Rayai, C., Bhinagawa,A., Yasunishi,A., Yoshino,M., Materston,R., Lander,E.S., Anglanda, M., Mallanda, C., Bhinagawa,A., Yasunishi,A., Yoshino,M., Materston,R., Lander,E.S., Anglanda, M., Mallanda, M., Materston,R., Lander,E.D., Anglanda, M., Mallanda, M., Wallanda, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              353 bp mRNA linear EST 11-DEC-2002
BY337247 RIKEN full-length enriched, whole joints Mus musculus cDNA
Glone L230006D15 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTAATGTGATCCCCCCCCTTTCCTTTCTCGTAGCCTGACGCGCAGCAGCCGCTTT 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 TCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                 3 CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA 62
                               /tissue_type="whole joints"
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                                                                                                                                                                                                          Score 33; DB 5
Pred. No. 9.2;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 AGGCGCCCGTCCCGCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 GACAGAGCGTCCCGCTTCCCTCC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
/clone="L230014G21"
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Nature 420, 563-573 (2002)
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51.7%;
                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                  Query Match
Best Local Similarity
----- 75; Conserva
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KEYWORDS
SOURCE
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BY337247
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                  Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Sihonga, A., Osato, N., Saito, R., Hill, D. P., Bult, C., Chrim, I., M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Chothia, C., Cobani, L.E., Cousine, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Gough, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V. Lee, Y., Lennard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pertea, G., Petrovsky, N., Pillaik, P., Portea, G., Petrovsky, N., Pillaik, R., Pontius, Jul., Qi, D., Ramachandran, S., Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandellin, A., Schneider, C., Semple, C.A., Setou, M., Shinada, K., Sultana, R., Takenaka, Y., Takenaka, Y., Takenaka, Y., Takenaka, Y., Takenaka, Y., Tawajin, N., Hirozane-Kishikawa, T., Yang, I., Yuan, Z., Zamer, A., Yang, I., Yuan, Z., Sandellin, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Nikaka, T., Fukuda, S., Hara, A., Hashizune, W., Inotani, R., Sakazune, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, I., Hirozane-Kishikawa, T., Yang, I., Sakazune, N., Sato, K., Shiraki, T., Waki, K., Sasaki, D., Salona, M., Sato, W., Shiraki, Y., Sasaki, J., Sakai, K., Sasaki, J., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNs.
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Aizawa.K., Akimura.T., Arakawa.T., Carninci,P., Fukuda,S.,
Hirozane.T., Indeani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
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encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
Fax: 81-45-503-9216
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Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
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Location/Qualifiers
1. .348
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COMMENT

TITLE

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source

FEATURES

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Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalo, X., Schriml, L.M., Kanapin, A., Matsuda, H., Entcher, C.F., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Garibodid, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustinnoich, S., Hirokawa, N., Jackson, I.J., Jarvis, B.D., Kanal, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.B., N., Magashima, T., Martais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrosky, N., Pillai, R., Pontrius, J.U., Qi, D., Kamachandran, S., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K., Yang, L., Wahlestedt, C., Wang, Y., Watenabe, Y., Wanger, L., Wahlestedt, C., Wang, Y., Watenabe, Y., Wang, L., Yang, L., Yang, L., Wahlestedt, C., Wang, Y., Watenabe, Y., Yang, L., Wahlestedt, C., Wang, Y., Watenabe, Y., Kang, L., Yang, L., Wahlestedt, C., Wang, Y., Watenabe, Y., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Satawa, T., Pukuda, S., Hara, A., Hashizune, W., Imctani, R., Ishi, Y., Itch, M., Kagawa, I., Myazaki, A., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rugers, J., Birney, B. and Hayashizaki, Y., Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIGURE Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopediar real-time sequence clustering for construction of a nonredundant cDNA library Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Expropration of security and schore Exploration of security of Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physica and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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                                        Email: genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,
Hirozani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,
Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,
Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,
Shizaki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and
Hayashizaki, T. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Namm. Genome. 12, 673-677 (2001)
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10 (11), 1757-1771 (2000)
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cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 354)
Okazaki, Y. Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,
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Ne Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Alazawa,Y., Akimura,T., Arakkawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
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Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper selected cDNAs to prepare full-length cDNA libraries for rapper selected cDNAs to prepare full-length cDNA libraries for rapper selected cDNAs to prepare full-length cDNA libraries for rapper sequencer. Genome Res. 10 (10), 1617-1630 (2000)

RIKBN integrated sequence analysis (RISA) system--184-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence Clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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BY343718 RIKEN full-length enriched, whole joints Mus musculus cDNA
clone L230047A12 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prepare mouse tissues.

Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.
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Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Sauvki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalla,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gasterland,T.
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/tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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/mol_type="mRNA"
/db_xref="taxon:10090"
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Best Local Similarity 51.7%;
Matches 75; Conservative (
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62

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Mammalia burneria; Rodentia; Sciurognath; Muridae; Murinae; Muser Banderia; Eurobach; V. Rasukawa T., Adachi, J., Bono, H., Kondo, S., Nikaido, T., Osato, N., Saito, R., Buzuki, H., Yamanaka, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T. Baldarelli, R., Hill, D. P., Bult, C., Hume, D.A., Quasckenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V., Beter, C.F., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboddi, M., Gissi, C., Godzik, A., Gausterland, T., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A., Kurochkin, I.V. Lee, Y., Lenhard, B., L., Wons, P.A., Maglott, D. R., Namathin, I.V. Lee, Y., Lenhard, B., L., Wons, P.A., Maglott, D., Rawaji, H., Kawasawa, Y., Leharda, B., L., Miki, H., Nagashima, T., Numata, K., Okido, T., Perces, G., Petrovsky, N., Pellais, L., McChioni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Perce, G., Petrovsky, N., Pellais, W., Shneider, C., Semple, C.A., Setou, M., Shimada, K., Saltani, A., Schoeider, C., Semple, C.A., Yanagisawa, Y., Takenaka, Y., Pukuda, S., Marah, Boris, A., Yanagisawa, M., Yasunishi, A., Sato, K., Shiraki, T., Waki, K., Kawai, J., Niyazaki, A., Hashizume, W., Inctana, K., Sato, K., Shiraki, Y., Malayasaka, J., Ragama, J., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shiragawa, A., Yasunishi, A., Yashinagawa, Y., Yasunishi, A., Yashinagawa, Yasunishi, A., Yashina, Y., Shiraki, Y., Arakawa, T., Mayazaki, Y., Sasaki, W., Inctional annotation of 60,770 full-length cDNAs
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
                                                                                3 CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA
                                                                                                                                                                                                                                                                                 63 TCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCAJGCGCGTGACCGGACACG
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AUTHORS
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Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King B.L., Konagaya, R.,
Kurochkin, I.V., Lee, Y., Ledard, B.L., Konagaya, R.,
Kurochkin, I.V., Lee, Y., Lendard, B.L., Nongeshima, T.,
Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,
Nummata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,
Petrovaky, N., Pillai, R., Pontius, Ju., Reid, J., Ring, B.E., Ringwald, M.,
Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Tasdala, R.D., Tomita, M.,
Verardo, R., Wanger, L., Wahlestedt, C., Wang, Y., Watcanabe, Y.,
Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carnini, P.,
Hayatsu, N., Hirozane-Kishikawa, T., Komno, H., Nakamura, M.,
Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,
Itoh, M., Kagawa, I., Miyazaki, A., Sasaki, D., Shibata, K.,
Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,
Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
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1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-922
Fax: 81-45-503-9216
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to
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/clone_lib="RIKEN full-length enriched, whole joints"
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/db_xref="taxon:10090"
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JOURNAL MEDLINE PUBMED COMMENT

TITLE

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Gaps ; 0

18.6%; Score 33; DB 5; Length 360; 51.7%; Pred. No. 9.2; cive 0; Mismatches 70; Indels

Conservative

Best Local Similarity Matches 75; Conserv

Query Match

source

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                    Human Genome Sequences Mann. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia: Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 07-DEC-2002
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues.

Tissues were provided by Vassilis Aidinis (Biomedical Sciences Research Center 'Al. Fleming' Institute of Immunology 14-16 Al. Fleming street 16672 Vari, Greece ) whose assistance we gratefully acknowledge.

Please visit our web site (http://genome.gsc.riken.go.jp) for
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Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A.,
Computational Analysis of Full-Length Mouse cDNAs Compared with
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BY083658 RIKEN full-length enriched, 10 days neonate heart Mus musculus cDNA clone K630044L13 5', mRNA sequence.
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/clone_lib="RIKEN full-length enriched, whole joints"
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Pred. No. 9.2;
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/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219 GACAGAGCGTCCCGCTCTCC 243
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Mus musculus
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Rogers,J., Birney,E. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-resegsc riken.jp, URL:http://genome.gsc.riken.jp/
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Shiraki,T., Tagani,M., Waki,K., Watahiki,A., Muramarsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of Cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rappd discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequence din Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
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/dev_stage="10 days neonate"
/clone_lib="RIKEN full-length enriched, 10 days neonate
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Please visit our web site (http://genome.gsc.riken.go.jp) for
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-Loc 75; Conserva
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/note="with the content of the conte
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Fax: (204) 983-4604
Bmail: scloutier/agr.gc.ca
was cloned directionally, not all sequences generated with reverse
primer where from the 5' end (same with forward primer and 3'end).
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Wararyota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Pooideae, Triticeae, Triticum.
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                                                                                                                                                                                                                                                                                                                                          63 TCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                     109 CCTCACCAGCTCGCACTCTCCTCGGGGCCGCACGGCTCGCCGTGCCCCTGCCCACCACGG 168
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                                                                                                                                                                                                                 3 CTTATCGTGACAGGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloudier, S., Dong, G. and Walsh, A.
Wheat functional genomics - Thatcher Lr1 cDNA library
Unpublished (2001)
Contact: Dr. Sylvie Cloutier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
                                                                                                                                                      ö
                                                                                           Length 611;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 621;
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51.7%; Pred. No. 9.3;
                                                                                           DB 7;
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                                                                                     Score 33; DB 7
Pred. No. 9.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/cultivar="Thatcher Lr1"
/db xref="taxon:4565"
/clone="Talr1138G03F"
/tissue_type="Leaf tissue"
/dev stage="14 Days old"
/lab_host="E, coli XLOLR"
constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Average insert size is >2.2kb
Plate: 138 row: G column: 03
Seg primer: M13 Forward.
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BQ620008.1 GI:21625087
                                                                                        Query Match
Best Local Similarity 51.7%;
Matches 75; Conservative
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Best Local Similarity
Matches 75; Conserv
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BQ620008
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 611) Piao, Y., Ko,N.T., Lim,M.K. and Ko,M.S.H. Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                     171 CCTCACCAGCTCGCACTCTCCTCGGGGGCGCACGGCTCGCCGTGCCCTGCCCACCACGG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                          TCGGAACAGGACGCCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACG
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National Institutes of Health
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
Plate: B0991 row: A column: 12
Seg primer: M13 Reverse
High quality sequence stop: 611
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dev stage="Unfertilized Egg"
lab_host="DH108"
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strain="CS7BL/6J"
db_xref="niasS::B0991A12-5"
db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 11 (9), 1553-1558 (2001)
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organism="Mus musculus"
                                                                                                                                               123 AGGCGCCCGTCCCGCTTATCGCGCC 147
                                                                                                                                                                                                          231 gacadadcdrccccrrrcccrcrcc 255
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Mus musculus
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CF916169
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KEYWORDS
SOURCE
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/dev stage="adult"
//dev stage="adult"
/lab_host="DH10B"
/clone_llb="Sugano mouse kidney mkia"
/clone_llb="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME185-FL3; Site 1: DraIII
/note="Organ: kidney; Vector: pmE185-FL3; Site 1: DraIII
(CACTGTGGTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTTGGCTAGTGG], digested
and cloned into distinct DraIII sites of the pME185-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW319335
635 bp mRNA linear EST 25-JAN-2000 unlifed.yl Sugano mouse kidhey mkia Mus musculus cDNA clone IMAGE:2395039 5' similar to TR:Q9YGP5 Q9YGP5 RRM-TYPE RNA-BINDING PROTEIN HERMES. ; mRNA sequence.
                                                                                                                                                                                                                                                                                     63 TCGGAACAGGACGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
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Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Moderwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., The Wash Unous EST Project 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                       93 CCTCACCAGCTCGCACTCTCCTCGGGGCGCACGGCTCGCCGTGCCCCTGCCCACCACGG 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                               3 CTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTA
                                                                                                                                                                                                                              33 ciraardidarcccccccccrrrcirrcrrrccaraccraaccccccaccacrrr
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TTE1: 314 286 1800
Fax: 314 286 1810
                                                                                                                              .;
0
                                                                            7; Length 624;
constructed by Yulan Piao."
                                                                            DB
                                                                                                                           0; Mismatches
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                                                                          18.6%; Score 33;
51.7%; Pred. No.
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High quality sequence stop: 305.
Location/Qualifiers
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/clone="IMAGE:2395039"
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Mus musculus
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/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW319335.1 GI:6748879
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                                                                                                  Local Similarity 51.7% tes 75; Conservative
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                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Site_2: Not1; Mouse cDNA project by the Laboratory of Genetics, National Institute on Asing (NIA), Intramural Research Program, NIH (http://lgam.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 1488 unfertilized eggs. Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                           EST 05-NOV-2003
                                                                                                                                                                                                                                                                                                        CF913548 624 bp mRNA linear EST 05-NOV-2003
B0950D02-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus
musculus cDNA clone NIA:B0950D02 IMAGE:30477061 5', mRNA sequence.
                   CCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGGTCCCGCTTA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                                                                 'note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: SalI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Genetics
National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsui.grc.nia.nih.gov
Plate: B0950 row: D column: 02
Seq primer: M13 Reverse
High quality sequence stop: 624
POLYA=No.
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/db_xref="taxon:10090"
/clone="N1A:80950D02 IMAGE:30477061"
/dev_stage="Unfertilized E9g"
/lab_host="DH108"
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                                                                                                                                                                          555 CGCCACGAGGCGCCACAGAAGGCAA 579
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                                                                                                                        141 TCGCGCCTATAAATACAGCCCGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Dawood B. Dudekula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                   CF913548
CF913548.1 GI:38184750
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KEYWORDS
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CF913548
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COMMENT

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Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGCACA."
                                                                                                                                                                                                                                                                   63 TCGGAACAGGACGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                              98 CTCACCAGCTGCACTCTCTGGGGGGGCACGGCTGGCGTGGCCCTGCCCACCACGG 157
                                                                                                                                                                                  Query Match 18.6%; Score 33; DB 2; Length 635; Best Local Similarity 51.7%; Pred. No. 9.3; Matches 75; Conservative 0; Mismatches 70; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                 123 AGGCGCCCGTCCCGCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                                                                                                             158 GACAGAGGGTCCCGCTTCCCTCC 182
                                                               ORIGIN
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Search completed: October 24, 2005, 21:53:24 Job time : 1285.71 secs

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AAX6698 Human neu Abk90730 CDNA enco AAX6698 Human neu Abk90731 CDNA enco Adt43165 Bacterial Aca45469 Prokaryot Ad127170 Human gen Ada03092 Human LFN Ada6376 Human LFN

Adb72830 Human LFN Acn43958 Human gen Aac23731 Human sec

Abl19245 Drosophil Abl19244 Drosophil Ada01209 Human col Ad45695 Bacterial Abd13766 Pseudomon Ach89781 Human gen Acs17480 DNA encod Acs151490 Pseudomon Aca13495 Prokaryot Ad56860 Bacterial Abd13493 Pseudomon Abd13493 Pseudomon Abd13431 Pseudomon Abd13531 Pseudomon

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Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; OpIE2 promoter.
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ABD13766
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AAS51490
ACA19456
ADS56860
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ABD13633
AAX06989
ABK90730
AAX06988
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ADT43165
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ACN43958
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26-JUL-2002; 2002US-0396617P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OpIE2 promoter DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ48575 standard; DNA; 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BENNETT R P. WELCH P J. HARWOOD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPI; 2004-132944/13.
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FRIMPONG K.
FRANKE K E.
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                                  ADQ48575;
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Add48575 OpIE2 pro
Aav62487 O. pseudo
Aal613106 ps20p2F e
Add48539 Viral vec
Add48576 Viral vec
Aaa02474 Human col
Abl27503 Drosophil
Abl18800 Drosophil
Abl27502 Drosophil
Abl27502 Brosophil
Abl27502 Brosophil
Add47056 Bacterial
Add47086 Bacterial
Add404088 Pseudomon
Add89385 Oligonucl
Ads89483 Oligonucl
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Abl70389 Chemicall
Aas61341 Human gen
Adf83430 Bread whe
                                                                                                                            ; Search time 193.335 Seconds (without alignments) 5419.578 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              4390206 segs, 2959870667 residues
                                                                                                                                                                                                         US-09-896-888A-1_COPY_351_527
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                                                                                                                              October 24, 2005, 18:39:18;
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Maximum Match 100%
Listing first 45 summaries
                                                                                           nucleic search, using sw model
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AAV62487
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Maximum DB
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Franke KE;

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                                                                                 portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of
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                                                                                                                                                                                                                                                                          invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTTATCGTGACAGGACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCT 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATCGGAACAGGACGCCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACA 474
                                                                                                                                          undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a precombinant virus, generating replication-defective particles, and are useful as gene therapy vectors. The nucleic acid of the invention is also useful for producing and expression of one or more genes in an organism, and are useful for producing and expressing fusion polypeptides. The present DNA sequence represents the OpiE2 promoter that was used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Expression vectors for transforming insect cells from disparate lines - useful to express heterologous DNA, e.g. to allow study of gene
                                                           The invention comprises a nucleic acid molecule consisting of all or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pseudotsugata multicapsid nucleopolyhedrosis virus ie2 promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 177; DB 12; Length 560; 100.0%; Pred. No. 2.6e-48;
                                                                                                                                                                                                                                                                                                                                                                               Sequence 560 BP; 144 A; 156 C; 116 G; 144 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Orgyia pseudotsugata; polyhedrosis virus.
                   Disclosure; Fig 16; 555pp; English
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98CA-02221819.
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(first entry)
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Matches 177; Conservative
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19-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        475
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV62487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A STATE OF THE STATE OF T
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that comprises: (1) prokaryottic origin of replication; (1) insect carputes that comprises: (1) prokaryottic origin of replication; (1) insect arrows that homology to, and capable of functioning as, an immediate carly baculovirus promoter; (iii) prokaryotic promoter sequence, and (iv) selectable marker capable of conferring resistance to a bleomycin, or in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) cells with heterologus DNA, useful to allow study of gene expression and direct expression of heterologous gene products e.g. commercially important proteins. They are especially useful to allow expression of the heterologous melanotransferring, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transformation of insect cell inse from disparate species, allowing screening of lines for optimum post-translational modification of particular proteins. Shuttle vectors (urther comprising DNA transposable elements defining a transposon can be used to optimise heterologous protein expression and facilitate selection of desired transformants. (Updated on 17-OCT-2003 to standardise OS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease; tumour necrosis factor alpha; gene therapy; arthritis; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGAGGCGCCCGTCTCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                             This represents a Orgyia pseudotsugata multicapsid nucleopolyhedrosis virus (OpMNPV) immediate early 2 (Op ie2) promoter sequence. The invention provides a new shuttle vector for transforming insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 564;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 564 BP; 147 A; 160 C; 116 G; 141 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
expression and produce commercially important proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 177; DB 2;
Best Local Similarity 100.0%; Pred. No. 2.6e-48;
Matches 177; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              p2ZOp2F expression vector for insect cells.
                                    Claim 10; Page 82; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL61306 standard; DNA; 2773 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-NOV-2002; 2002WO-DK000764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-NOV-2001; 2001DK-00001702.
16-NOV-2001; 2001US-0331575P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KLYSNER S.
NIELSEN F S.
BRATT T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHARMEXA AS
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(NIEL/)
(BRAT/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PHAR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ield)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 3
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Frimpong K,

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The invention comprises a nucleic acid molecule consisting of all or a portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of undergoing recombination with a compatible recombination site in the presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful for producing and expressing fusion polypeptides. The present DNA sequence represents a plasmid that was used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 TATCGGAACAGGGCCTCCATATCAGCCGCGCTTATCTCATGCACGTGACCGGACA 470
                                                                                                                                                                                                                                        Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGAGGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; plasmid; recombination region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  351 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GICTIAICGIGACACACACCCAGCTICCIGIGITGCTAACCGCAGCCGGACGCAACTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viral vector-related plasmid pIB/V5-His-DEST recombination region #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12; Length 5038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5038 BP; 1342 A; 1178 C; 1198 G; 1320 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           viral vector; recombination site; recombinant virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.1%; Score 175.4; DB 12 99.4%; Pred. No. 1.5e-47; vative 0; Mismatches 1;
                                                                                                       Madden K,
                                                                                                                                                                                                                                                                                                                                                                            Example 18; Page 395-403; 555pp; English.
                                                                                                       Harwood S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADQ48576 standard; DNA; 141 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002US-0396335P.
2002US-0398617P.
2002US-0427231P.
2003US-0456496P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-JUL-2003; 2003WO-US022437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 99.4 les 176; Conservative
                                                                                                       Bennett RP, Welch PJ,
                                                                                                                                                                           WPI; 2004-132944/13.
   (FRIM/) FRIMPONG K.
(FRAN/) FRANKE K E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO2004009768-A2
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26-JUL-2002; 2
19-NOV-2002; 2
24-MAR-2003; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unidentified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADQ48576
       THE SECTION OF THE SE
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                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to immunogenic analogues of multimeric proteins such as immunogenic variants of interleukin 5 (LL5) and tumour necrosis factor alpha (TNF, TNFalpha) and methods for production of immunogenic analogues. The immunogenic analogue is useful for preparing a composition for treating inflammatory diseases, e.g., arthritis. It is also used in gene therapy. The present sequence is p220p2F expression vector for insect cells. This sequence is used to illustrate the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           415 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCTCATGCGCGTGACCGGACA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                    New immunogenic analogue of a polymeric protein, useful for preparing a composition for treating inflammatory diseases e.g. arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viral vector; recombination site; recombinant virus; replication-defective particle generation; gene expression inhibition; gene therapy vector; ds; plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      475 CGAGGCGCCCTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GTCTTATCGTGACGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2773 BP; 669 A; 750 C; 673 G; 681 T; 0 U; 0 Other;
                                                                                                       Mouritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 177; DB 9; Length 2
Best Local Similarity 100.0%; Pred. No. 3.86-48;
O Mismatches 0; Indels
                                                                                                   Voldborg B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viral vector-related plasmid - pIB/V5-His-DEST
                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 195-196; 196pp; English.
                                                                                                   Bratt T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
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26-JUL-2002; 2002US-0396677P.
19-NOV-2002; 2002US-0427231P.
24-MAR-2003; 2003US-0456496P.
03-JUN-2003; 2003US-0474940P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADQ48539 standard; DNA; 5038
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BENNETT R P.
WELCH P J.
HARWOOD S.
                                                                                                   Klysner S, Nielsen FS,
(VOLD/) VOLDBORG B. (MOUR/) MOURITSEN S.
                                                                                                                                                                    WPI; 2003-449558/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MADDEN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004009768-A2.
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ADQ48539 RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37 TAAGATCGNGCC 26
                                                Williams II, Bscower, Reinhard C, Giese K, F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster.
                                                              Escobedo
                                                                                                  Leshkowitz D, Kita D,
                        (CHIR ) CHIRON CORP.
                                                                                                                          WPI; 2000-126369/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200171042-A2
  27-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                            portion of one or more viral/baculoviral genomes and further containing at least two recombination sites that do not substantially recombine with each other. One or more of the recombination sites is capable of presence of one or more proteins active in lambda recombination. The presence of one or more proteins active in lambda recombination. The nucleic acid of the invention replicates in prokaryotic and eukaryotic cells. The nucleic acid of the invention is useful for constructing a recombinant virus, generating replication-defective particles, preventing/inhibiting the expression of one or more genes in an organism, and are useful for producing and expressing fusion polypeptides. The invention is also useful for producing and expressing fusion polypeptides. The present DNA sequence represents a recombination region of a plasmid that was used in the exemplification of the invention.
                                                                                                                                                                        Novel nucleic acid molecule comprising all or a portion of one or more viral genome and further comprising two or more recombination sites that do not substantially recombine with each other, useful as gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer; tumour; diagnosis; gene expression product; probe; detection; cancerous state; metastasis; identification; breast cancer; oestrogen receptor-positive breast cancer; therapy; coestrogen receptor-negative breast cancer; lung cancer; ss.
                                                                                                                                                                                                                                                    The invention comprises a nucleic acid molecule consisting of all or a
                                                                                                                          Franke KE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human colon cancer cell line polynucleotide sequence SEQ ID NO:2465.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.2%; Score 41; DB 12; Length 141; 100.0%; Pred. No. 0.0014; Live 0; Mismatches 0; Indels
                                                                                                                          Frimpong K,
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 141 BP; 43 A; 36 C; 27 G; 34 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 CITATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTTATCGCGCTATAAATACAGCCCGCAACGATCTGGTAAA 41
                                                                                                                         Madden K,
                                                                                                                         Harwood S,
                                                                                                                                                                                                                           Disclosure; Fig 17; 555pp; English
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98US-0085537P.
98US-0085696P.
98US-0105234P.
03-JUN-2003; 2003US-0474940P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA02474 standard; cDNA; 921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                      INVITROGEN CORP.
BENNETT R P.
WELCH P J.
HARWOOD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                         Sennett RP, Welch PJ,
                                                                                                                                                  WPI; 2004-132944/13.
                                                                       MADDEN K.
FRIMPONG K.
FRANKE K E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
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15-MAY-1998;
21-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA02474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                               (WELC/)
                                                                       (MADD/)
(FRIM/)
                                                                                                (FRAN/)
                                  (BENN/)
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Matches
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libraries constructed from human colon cancer cell lines. The present invention also describes a method of detecting differentially expressed genes correlated with a cancerous state of a mammalian cell, comprising detecting at least one differentially expressed gene product in a test sample derived from a cell suspected of being cancerous, where detection of the differentially expressed gene product is correlated with a cancerous state of the cell from which the test sample was derived. The polymucleotides sequences can be used in a method for detecting in differentially expressed genes correlated with a cancerous state of a mammalian cell. The polymucleotides can also be used as probes for detecting and mapping related genes. They can be used in diagnosis and prognosis of diseases and disorders (e.g. identification of premeastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). This is particularly for breast cancer, oestrogen receptor-positive breast cancer, oestrogen receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 CGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACGAGGCGCCCCGTCCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16 GACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 GGCGTCNAANCCACCTTCCCTTCGTCTCCGCGCTCCGCGTTCAGGGAGCGACTGTCCT 38
                                                                                                Labat I;
                                                                                                                                                                                                                                                                                                                             Polynucleotide library used to determine cancerous states of mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sudduth-Klinger J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                      Randazzo F, Kennedy GC, Pot D, Kassam A,
Crkvenjakov R, Dickson M, Drmanac S, Lab
Garcia V, Jones LM, Stache-Crain B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA00010 to AAA02716 represent polynucleotides isolated from cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developmental biology; cell signalling; insecticide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genomic polynucleotide SEQ ID NO 7876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 921 BP; 239 A; 214 C; 205 G; 223 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 18.1%; Score 32; DB 3; Length 921; 1 Similarity 51.5%; Pred. No. 2.1; 68; Conservative 0; Mismatcher 64. Thanh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           negative breast cancer, lung cancer, and colon cancer
Garcia PD,
              Innis MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 989; 1097pp; English.
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Gaps

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention
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                                                                                                                                       The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher weakayotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA ABR2072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
  New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genomic polynucleotide SEQ ID NO 33979.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 30.8; DB 4; Length 1342; Pred. No. 5.7; 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1342 BP; 324 A; 347 C; 372 G; 299 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77 GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      791 ĠTTGGĊACATTGĠĊĊATAĊAAATCĊŢĊAĠĠTCĊCAĠĠAAĠTÄĊĠAĠ 836
                                                                                            Claim 1; SEQ ID NO 33982; 21pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                        from WIPO at ftp.wipo.int/pub/published_pct_sequences
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ID ABL27502 standard; DNA; 3448 BP
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity 55.79
Matches 59; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511).

ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
                                                                                                                                                                                                                                                                detection reagent for detecting 1000 or more for elucidating cell signaling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 17.4%; Score 30.8; DB 4; Length 1268; Similarity 55.7%; Pred. No. 5.6; 59; Conservative 0; Mismatches 47; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1268 BP; 295 A; 336 C; 360 G; 277 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        717 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 762
                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 7876; 21pp + Sequence Listing; English
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                                                                                                                                                                Myers EW
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                                          23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
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11-JUL-2000; 2000US-00614150.
23-MAR-2001; 2001WO-US009231
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                                                                                                                                                                                                                                                             New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                Venter JC, Adams M,
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                                                                                                                 (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                          interactions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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RESULT 8 ABL27503

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
                    sequences [ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                        17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                   Gaps
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
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0
                                                                                                                                                       Score 30.8; DB 4; Length 3448; Pred. No. 7.1; 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster genomic polynucleotide SEQ ID NO 7873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.4%; Score 30.8; DB 4; Length 3600; illarity 55.7%; Pred. No. 7.2; Conservative 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                         1607 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 1562
                                                                                                                                                                                                                                                                                                                  77 GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                     Sequence 3448 BP; 894 A; 817 C; 801 G; 936 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3600 BP; 946 A; 856 C; 823 G; 975 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 7873; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ξ
Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Li PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL18800 standard; DNA; 3600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                            17.4%;
55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                        Local Similarity 55.7
nes 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
<sub>(</sub>Matches 59; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jenter JC,
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABL18800;
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL18800
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Gaps

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47; Indels

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                             1667 ACAACAGCTTCCGGTGGAGGTGCCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to novel recombinant carcinoma-associated protein (CAP) useful for screening a bioactive agent capable of binding to carcinoma associated (CA) protein and for evaluating the effect of a candidate correction are in screening methods and provides compositions for use in screening methods and provides compositions and methods associated with altered expression of TBX21 in cancer. Sultable cancers which can be diagnosed or screened by the invention includes actina cell carcinoma, fibrosarcoma, Kaposi's sarcoma, breast cancer and the present sequence is human carcinoma-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 GACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel recombinant carcinoma-associated protein such as mouse or human TBX21 protein, useful for screening a bioactive agent capable of binding to carcinoma associated protein, and for evaluating the effect of a candidate carcinoma drug.
                                                                                                                                                                                                                                                                                                                               Carcinoma-associated protein; CAP; acinar cell carcinoma; fibrosarcoma; Kaposi's sarcoma; breast cancer; Hairy cell leukaemia; human; ds.
17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29169 BP; 5725 A; 7553 C; 7224 G; 8641 T; 0 U; 26 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 29169;
                                                                                                    1607 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                     GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.4%; Score 30.8; D 61.0%; Pred. No. 12; ive 0; Mismatches
                                                                                                                                                                                                                                                                                                  Human carcinoma-associated (CA) gene TBX21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure, SEQ ID NO 4; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9042 cccccrccccccccccccc 9063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 GGACGCGCCTCCATATCAGCCG 92
                                                                                                                                                                                           AAD64735 standard; DNA; 29169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-DEC-2000; 2000US-00747377.
02-MAR-2001; 2001US-00798586.
08-NOV-2001; 2001US-00052482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-MAR-2002; 2002US-00105613
                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Engelhard EK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-874605/81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MORR/) MORRIS D W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 50; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                         US2003099963-A1.
                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                 11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-MAY-2003
                                                                   11
                                                                                                                                                                                                                              AAD64735;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                          RESULT 11
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Gaps

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Length 1404;

Score 30.6; DB 13; Pred. No. 6.7; 0; Mismatches 29;

17.3%;

Query Match

Conservative

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New recombinant DNA construct comprising a promoter positioned to provide for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
                                                                                             Recombinant DNA construct, transformed plant; improved plant property; cold tolerance, heat tolerance, drought tolerance; herbicide, osmosis; pathogen tolerance; pest tolerance; plant disease resistance; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polymucleotide; gene; ss.
                                                                                                                                                                                                                                                                                                                                              Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 45503; 122pp; English.
                                                                                                                                                                                                                                                                                                                                             Chen X,
                  ADT47065 standard; cDNA; 1404 BP.
                                                                             Bacterial polynucleotide #21816.
                                                                                                                                                                                                                                                                                                                                             Hinkle GJ, Slater SC,
                                                                                                                                                                                                                                           20-FEB-2003; 2003US-00369493
                                                                                                                                                                                                                                                              21 - FEB=2002; 2002US-0360039P
                                                         (first entry)
                                                                                                                                                                                                                                                                                           HINKLE G J.
SLATER S C.
                                                                                                                                                                                                                                                                                                                         GOLDMAN B S.
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-061375/06.
                                                                                                                                                                                                   US2003233675-A1.
                                                                                                                                                                                                                                                                                                                 CHEN X.
                                                          02-DEC-2004
                                                                                                                                                                                                                        18-DEC-2003
                                      ADT47065;
                                                                                                                                                                                Bacteria
                                                                                                                                                                                                                                                                                            (HINK/) 1 (SLAT/) (CHEN/) (GOLD/)
                                                                                                                                                                                                                                                                                  (CAOY/)
                                                                                                                                                                                                                                                                                                                                             Cao Y,
RESULT 12
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The invention relates to a recombinant DNA construct comprising a promoter functional in a plant cell, where the promoter is positioned to provide for expression of a polynuclectide encoding a polypeptide from a microbial source. The invention also relates to a transformed plant comprising the recombinant DNA construct and a method of producing a transformed plant having an improved property. The plant is a crop plant such as maize or soybean. The method of producing a transformed plant the ecombinant DNA construct and growing the transformed plant where the polynucleotide or polypeptide is useful for improved plant where the polynucleotide or polypeptide is useful for improved plant properties, e.g. improved cold, heat or drought tolerance, tolerance to herbicides, extreme osmotic conditions, pathogens or pests, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, by modification of photosynthesis or by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            providing improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan production. This sequence represents a bacterial polynucleotide used in the scope of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at sequance.
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Sequence 1404 BP; 236 A; 489 C; 454 G; 225 T; 0 U; 0 Other;
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encoding fragment or reverse complement), comprising a nucleotide sequence encoding a polypeptide comprising an amino acid sequence involved in or associated with the biosynthesis of isoprenoids in a rice plant. Also included are an isolated polypeptide involved in or associated with the biosynthesis of isoprenoids in a plant, an expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotides and polypeptides associated with isoprenoid synthesis in plants, useful for producing transgenic plants, for targeted gene disruption, as well as markers or probes.
                                         99 ATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAG 158
                                                                  523
                                                                                                                                                                                                                                                                                                   isoprenoid biosynthesis; ss; isopentenyl diphosphate; IPP; dimethylallyl alcohol; DMAPP; short-chain plastid prenyltransferase; gibberellin; carotenoid; abscisic acid; tocopherol; plastoguinone; phylloquinone; mevalonate pathway; phytosterol; brassinosteroid; ubiquinone; monterpene; sesquiterpene; protein prenylation; chlorophyll; haeme; yield.
                                                                  464 Accechadedecidadacenecedanoneanecidececinecedecenineegecaage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a polynucleotide (or its complement, protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         B, Glazebrook J;
Provart N, Ricke
                                                                                                                                                                                                                                                                                 Plant isoprenoid biosynthesis-associated DNA #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ghassemian M, Briggs SP, Cooper B
Katagiri F, Kreps J, Moughamer T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 563; 117pp; English
                                                                                                                                                                                                ВР
                                                                                              159 CCCGCAACGATCTGGTA 175
                                                                                                                          524 ACCGCGACGATCTGGAA 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-2001; 2001US-0325277P.
04-APR-2002; 2002US-0370620P.
04-APR-2002; 2002US-0370743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-SEP-2002; 2002US-00259194.
                                                                                                                                                                                              ADI45632 standard; DNA; 657
                                                                                                                                                                                                                                                       22-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LANGE B M.
GHASSEMIAN M.
BRIGGS S P.
COOPER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLAZEBROOK J.
GOFF S A.
KATAGIRI F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KREPS J.
MOUGHAMER T.
PROVART N.
RICKE D.
ZHU T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-090562/09.
Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                           US2004010815-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lange BM,
Goff SA,
Zhu T;
                                                                                                                                                                                                                           AD145632;
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(MOUG/)
(PROV/)
(RICK/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (LANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GHAS/)
(BRIG/)
(COOP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GLAZ/)
(GOFF/)
                                                                                                                                                                    RESULT 13
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cassette. Comprising the polymuciacitie, a nost cell confirming the cassette. The polypeptides and polymucleotides include those associated with the biosynthesis of isopencenyl diphosphate (IPP) and dimethylallyl alcohol (DMAPP), the biosynthesis of short-chain plastid confirming the biosynthesis of short-chain plastid preparases, the biosynthesis of short-chain plastid preparation of the biosynthesis of carotenoids and/or abscisic acids, the biosynthesis of tocopherols, plastoquinone and/or phylloquinone biosynthesis of tocopherols, phystosterol and brassinosteroid metabolism, biosynthesis of ubiquinone, biosynthesis of monteropenes and sequiterpenes, protein prenylation, and biosynthesis of chlorophyll or haeme. Also disclosed are banana, wheat and corn homologues of some of the rice polymucleotides. The polymucleotides are useful for producing transgenic plants, where the genome is augmented by a nucleic acid molecule of the invention, or in which the corresponding gene has been disrupted, e.g. to result in a loss, a decrease or an alteration in the function of the product encoded by the gene. The plants may also have increased yields and/or produce a better quality product than the corresponding wild-type plant. The nucleic acid molecules are useful for targeted gene disruption, as well as markers and probes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGCGCCTCCATATCA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      format directly from USPTO at sequence. The present sequence segdata.uspto.gov/sequence.html?DocID=20040010815. The present sequence is an isoprenoid biosynthesis- associated DNA included in the sequence listing but not mentioned anywhere else in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTTCCCGCTTATCGCGC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGCATGATTGCGTGTTCTCGTGCCGGGTCTCGACGGGCCGGCTGGCCTCCCGCGC 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
comprising the polynucleatide, a host cell comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 16.9%; Score 30; DB 12; Length 657; I Similarity 53.4%; Pred. No. 8.9; 63; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 657 BP; 109 A; 257 C; 178 G; 113 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.9;
rhes 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa polynucleotide #12692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Deloughery C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0074788P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibacterial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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The invention relates to Pseudomonas aeruginosa polypeptides and the polymucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, of the ability to bind a P. aeruginosa uncleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant or production of P. aeruginosa derived peptides or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused infection, and in detection of P. aeruginosa sequences or other sequences of pseudomonas species using biochip technology Sequences ABD01397-ABD17867 represent P. aeruginosa polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but, was obtained in electronic format from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 CCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACGAGGCGCCCGTCCCGCTTA 140
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useful as molecular targets for diagnostics, prophylaxis and treatment of
pathological conditions resulting from bacterial infection.
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Marx A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ss; cell proliferative disorder; breast; methylation; cytostatic; gene therapy; single nucleotide polymorphism; SNP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 16.9%; Score 30; DB 11; Length 1710; Local Similarity 57.4%; Pred. No. 11; Los 54; Conservative 0; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1710 BP; 380 A; 455 C; 526 G; 349 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maier S, Martens J,
Schmitt M, Look MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          141 TCGCGCCTATAAATACAGCCCGCAACGATCTGGT 174
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                                                           Disclosure; SEQ ID NO 12692; 455pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koenig T,
Schmitt A,
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07-JAN-2003; 2003DE-01000096.
17-APR-2003; 2003DE-01017955.
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Nimmrich I, Rujan T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-348468/32.
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The invention relates to a novel method for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy comparising analysing the methylation pattern of a target nucleic acid by contacting at least one of the target nucleic acids in biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic activity, and may have a use in gene therapy. The set of oligonucleotides comprising at least two of the oligomers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within the sequences. The methods, nucleic acid, oligonucleotide, and kit are useful for the treatment, characterisation, classification and/or differentiation, of breast cell proliferative disorders. The method is also useful for the predicting the responsiveness of a subject with a cell proliferative disorders is used disorder of the breast tissues to a therapy. The present sequence is used in the exemplification of the invention.
                            Claim 25; SEQ ID NO 401; 104pp; English
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Sequence 3107 BP; 823 A; 120 C; 814 G; 1350 T; 0 U; 0 Other;

Gaps ö Match 16.9%; Score 30; DB 13; Length 3107; Local Similarity 50.7%; Pred. No. 13; les 72; Conservative 0; Mismatches 70; Indels (Query Match Best Loc Matches

2079 Aaceceaaaaccacceerecrecrecrecrecraceaceceeceaaraacereaceee 2020 66 GAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACGAGG 125 6 ATCGTGACAGGACGCCAGCTTCCTGTGTTACTAACGGCAGGCGGACGCAACTCCTTATCG 65 qq ò

2019 GAACCCGCGACTCTTCCTCATTTAAACAACTTCCTTAACGCGCCCGAACAAACGACCCG 1960

g ò

126 CGCCGTCCGCTTATCGCGC 147

1959 CACTTCCTCCAATATCGCGCC 1938

Search completed: October 24, 2005, 18:58:05 Job time: 199.335 secs

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Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Sequence 60, Appl
Sequence 12, Appl
Sequence 129, App
Sequence 149, App
Sequence 2538, Ap
Sequence 25442, A
Sequence 25442, A
Sequence 25442, A
Sequence 25441, A
Sequence 25441, A
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Sequence 45503, A
Sequence 45503, A
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Sequence 10, Appl
Sequence 26108, A
Sequence 7296, Ap
Sequence 7296, Ap
Sequence 7296, Ap
Sequence 7196, Ap
Sequence 7196, Ap
Sequence 71196, Ap
Sequence 6594, Ap
Sequence 6594, Ap
Sequence 22976, Appl
Sequence 22374, Ap
Sequence 7326, Appl
Sequence 22, Appl
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OTHER INFORMATION: Description of Artificial Sequence:Promoter
OTHER INFORMATION: sequence of the OpMNPV ie2 gene
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24 US-10-939-107-60
21 US-10-622-088-89
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23 US-10-622-088-127
24 US-10-622-088-149
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22 US-11-097-143-26108
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US-09-817-665-5
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Patent No. US20020116723A1
GENERAL INFORMATION:
GENERAL INFORMATION:
HAPLICANT: The University of British Columbia
TITLE OF INVENTION: Insect Expression Vectors
FILE REPERENCE: 80021-44
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR PLICATION NUMBER: US/09/048,911
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1998-03-26
PRIOR FILING DATE: 1997-03-27
NUMBER OF SEQ ID NOS: 50
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Best Local Similarity 100.
Matches 177; Conservative
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Sequence 126, App
Sequence 1, Appli
Sequence 60, Appl
Sequence 60, Appl
                                                                                                                                                                            October 24, 2005, 20:18:24; Search time 361.161 Seconds (without alignments) 4044.488 Million cell updates/sec
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1: /cgn2 6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2 6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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20: /cgn2 6
                                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-622-088-126
US-09-896-888A-1
7 US-10-255-074-60
11 US-10-846-911-60
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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APPLICANT: The University of British Columbia
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GREAKL INCOMMATION:
APPLICANT: Bennet, Robert P.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Ference, Steven
APPLICANT: Frankod, Steven
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.545007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT APPLICATION NUMBER: US 60/396,335
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR APPLICATION NUMBER: US 60/396,335
PRIOR PLING DATE: 2002-07-18
PRIOR PLING DATE: 2002-07-26
PRIOR PLING DATE: 2002-07-26
PRIOR PLING DATE: 2003-07-19
PRIOR PLING DATE: 2003-07-26
PRIOR PLING DATE: 2003-07-36
PRIOR PLING DATE: 2003-03-34
PRIOR FLING DATE: 2003-03-34
PRIOR PLING DATE: 2003-03-34
PRIOR FLING DATE: 2003-03-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) OTHER INFORMATION; OpiE2 promoter sequence US-10-622-088-126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 126, Application US/10622088 Publication No. US20040219516A1 GENERAL INFORMATION:
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ORGANISM: Unknown
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Sequence 1, Application US/09896888A Patent No. US20020116723A1 GENERAL INFORMATION:

US-09-896-888A-1

RESULT 3

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351 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 410
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Sequence 60, Application US/10295074

Publication No. US20030185845A1

Sequence 60, Application US/20295074

Publication No. US20030185845A1

SERVERAL INFORMATION:

APPLICANT: Pharmexa A/S

TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS

FILE REPERENCE: P10.13DK00

CURRENT FILING DATE: 2002-11-15

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 177; DB 9; Length 564; 100.0%; Pred. No. 2e-54;
TITLE OF INVENTION: Insect Expression Vectors
FILE REFERENCE: 80021-4
CURRENT APPLICATION NUMBER: US/09/896,888A
CURRENT FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US/09/048,911
PRIOR PILING DATE: 1998-03-26
PRIOR FILING DATE: 1997-03-27
PRIOR FILING DATE: 1997-03-27
NUMBER: PECENTIN NUMBER: 60/049,946
SOFTWARE: PECENTIN VECTOR OF SEQ ID NOS: 50
SOFTWARE: PECENTIN VECTOR OF SEQ ID NOS: 50
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LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Orgyia pseudotsugata
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OTHER INFORMATION: ECORI site
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LOCATION: (625).. (630)
OTHER INFORMATION: ClaI site
FEATURE:
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LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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Best Local Similarity 100.0
Matches 177; Conservative
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OTHER INFORMATION: BamHI
FEATURE:
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NAME/KEY: misc_recomb
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LENGTH: 2773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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355 GTCTTATCGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCT 414
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       OTHER INFORMATION: p2ZOp2F expression vector for insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 177; DB 21; Best Local Similarity 100.0%; Pred. No. 2.6e-54; Matches 177; Conservative 0; Mismatches 0;
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                           FEATURE:
NAME/KEY: misc_recomb
LOCATION: (561)..(566)
OTHER INFORMATION: HindIII site
                                                                                                                                                                                                                                          NAME/KEY: misc recomb
LOCATION: (586)..(591)
OTHER INFORMATION: ECORI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_recomb

LOCATION: (2551)..(2556)

CHER INFORMATION: Apal1 site

US-10-846-911-60
                                                                                                                                                                                                                                                                                                                                                               LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
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LOCATION: (1156)..(1161)
OTHER INFORMATION: Apall site
                                                                                                                                                                         LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc recomb
LOCATION: (625)..(630)
OTHER INFORMATION: Clal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (629)..(634)
OTHER INFORMATION: Clai site
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NAME/KEY: misc_recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: PEt1 site
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OTHER INFORMATION: NCOI site
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LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
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LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval,
                                                                                                                                             NAME/KEY: misc recomb LOCATION: (573)..(578
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LOCATION: (593)..(598
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LOCATION: (2204)..(22
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US-10-939-107-60
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US-10-846-911-60

US-10-846-911-60

Sequence 60, Application US/10846911

Publication No. US20040258660A1

GENERAL INFORMATION:

APPLICANT: KIYSNER, Steen

APPLICANT: NOLDBORG, Bionn

APPLICANT: WOLDBORG, Soren

APPLICANT: WOLDBORG, Soren

TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS

FILE REFERENCE: 674542-2018

CURRENT APPLICATION NUMBER: PCT/DK02/00764

PRIOR PLING DATE: 2002-11-16

PRIOR PLING DATE: 2001-11-16

PRIOR PLING DATE: 2001-11-16

PRIOR FILING DATE: 2001-11-16

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin version 3.1

SEQ ID NO 60

LENGTH: 2773

TAPER TATES APPLICATION NUMBER: PA 2001 01702

BENOR FILING DATE: 2001-11-16

LENGTH: 2773

TAPER TATES PATENTING DATE: 2001-11-16

LENGTH: 2773

TATES PATENTING DATE: 2001-11-16

LENGTH: 2773
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100.0%; Pred. No. 2.6e-54;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc recomb
LOCATION: (2551)..(2556)
COTHER INFORMATION: Apal1 site
US-10-295-074-60
                                                                                            NAME/KEY: misc recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: ApalI site
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ORGANIŚM: Artificial sequence
FEATURE:
                           LOCATION: (629)..(634)
OTHER INFORMATION: Clai site
                                                                                                                                                               FEATURE:
NAME/KEY: misc recomb
LOCATION: (2128)..(2133)
OTHER INFORMATION: P&LI site
                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: misc_recomb
LOCATION: (2204)..(2209)
OTHER INFORMATION: Ncol site
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LOCATION: (2284)..(2289)
OTHER INFORMATION: Aval site
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Best Local Similarity 100.
Matches 177; Conservative
NAME/KEY: misc recomb
LOCATION: (629)..(634
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Indels

Length 2773;

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61 TATCGGAACAGGACGCGCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACA 120
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                                                                                     415 TATCGGAACAGGCGCCTCCATATCAGCCGCGCTTATCTCATGCGCGCGGACA 474
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                                                                                                                                                                                                                                                                                                                                                                              475 CGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 531
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Publication No. US20040219516A1

GENERAL INPOMENTION:
APPLICANT: Welch, Peter J.
APPLICANT: Welch, Peter J.
APPLICANT: Wadden, Knut
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Konneth
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
FILE EFFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US 60/396,335
FRIOR APPLICATION NUMBER: US 60/396,617
FRIOR FILING DATE: 2002-07-26
FRIOR APPLICATION NUMBER: US 60/396,617
FRIOR FILING DATE: 2002-07-26
FRIOR APPLICATION NUMBER: US 60/427,231
FRIOR FILING DATE: 2003-07-18
FRIOR APPLICATION NUMBER: US 60/426,496
FRIOR APPLICATION NUMBER: US 60/426,496
FRIOR APPLICATION NUMBER: US 60/456,496
FRIOR APPLICATION US 60/456,496
FRIOR APPLICATION US 60/456,496
FRIOR APPLICATION US 60/456,496
FRIOR APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.1%; Score 175.4; DB 21; Length 5038; 99.4%; Pred. No. 1.1e-53; Live 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 8
US-10-622-088-127
i Sequence 127, Application US/10622088; Publication No. US20040219516A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: pIB/V5-His-DEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 99.4
Matches 176; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-622-088-89
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APPLICANT: Pedersen, Hans Rudolf
APPLICANT: Ebert, Bjarke
APPLICANT: Ebert, Bjarke
APPLICANT: Resmussen, Louise Henriette
APPLICANT: Rasmussen, Peter Birk
TITLE OF INVENTION: Novel Application of Vaccination Against TNF-alpha
FILE REFERENCE: 674542-2020
CURRENT APPLICATION NUMBER: 2004-00-10
PRIOR PILING DATE: 2004-09-10
PRIOR PLING DATE: 2003-03-11
PRIOR PLING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: 60/363,128
PRIOR PILING DATE: 2002-03-11
PRIOR PILING DATE: 2002-03-11
SPRIOR FILING DATE: 2002-03-11
SPRIOR PILING DATE: 2002-03-11
SPRIOR FILING DATE: 2007-03-11
SPRIOR APPLICATION NUMBER: 60/363,128
PRIOR FILING DATE: 2007-03-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2773;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: p2ZOp2F expression vector for insect cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 177; DB 24; Best Local Similarity 100.0%; Pred. No. 2.6e-54; Matches 177; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_recomb
LOCATION: (2294)..(2299)
OTHER INFORMATION: Aval, Smal, and Xmal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_recomb
LOCATION: (561)...(566)
OTHER INFORMATION: HindIII site
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc recomb
LOCATION: (593)..(598)
OTHER INFORMATION: BamHI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_recomb
LOCATION: (1156)..(1161)
OTHER INFORMATION: Apal site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_recomb

LOCATION: (2551)..(2556)

1 OTHER INFORMATION: ApaLI site

US-10-939-107-60
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LOCATION: (5867..(591)
OTHER INFORMATION: ECORI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial sequence
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LOCATION: (573)..(578)
OTHER INFORMATION: Aval site
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LOCATION: (625)..(630)
OTHER INFORMATION: ClaI site
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LOCATION: (629)..(634)
OTHER INFORMATION: ClaI site
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LOCATION: (2128)..(2133)
OTHER INFORMATION: PetI site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc recomb
LOCATION: (2284). (2289)
OTHER INFORMATION: Aval site
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LOCATION: (2204)..(2209)
OTHER INFORMATION: Ncol site
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Gaps ; 0

Indels

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OTHER INFORMATION: Recombination region of pIB/V5 His DEST
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                                                                                                                                                                                      FEATURE:
NAME/KEY: misc feature
LOCATION: (141)..(142)
OTHER INFORMATION: n is a, c, g,
SOFTWARE: Patentin version 3.2
SEQ ID NO 149
LENGTH: 325
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Best Local Similarity 61.24
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (145)..(276)
US-10-622-088-149
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; NAME/KEY: CDS
; LOCATION: (1)..(3138)
US-10-156-761-2538
                                                                                                          ORGANISM: Artificial FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-156-761-2538/c
                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
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US-10-156-761-1
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Sequence 149, Application US/10622088

Publication No. US20040219516A1

GENERAL INFORMATION:
APPLICANT: Bennett, Peter J.
APPLICANT: Harwood, Steven
APPLICANT: Harwood, Steven
APPLICANT: Franke, Kenneth
APPLICANT: BOG 3042.545001, 128

FILE REFERENCE: 0942.545001, 18

FRIOR APPLICATION NUMBER: US 60/396,335

FRIOR APPLICATION NUMBER: US 60/398,617

FRIOR APPLICATION NUMBER: US 60/427,231

FRIOR APPLICATION NUMBER: US 60/427,231

FRIOR APPLICATION NUMBER: US 60/456,496

FRIOR APPLICATION NUMBER: US 60/456,496

FRIOR APPLICATION NUMBER: US 60/474,940

FRIOR FILING DATE: 2003-00-03

FRIOR APPLICATION NUMBER: US 60/474,940
                                                                                       APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Frimpong, Kenneth
APPLICANT: Franke, Kenneth E.
TITLE OF INVENTION: Viral Vectors Containing Recombination Sites
FILE REFERENCE: 0942.5450007
CURRENT APPLICATION NUMBER: US/10/622,088
CURRENT FILING DATE: 2003-07-18
PRIOR FILING DATE: 2003-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR FILING DATE: 2002-07-18
PRIOR PRILOR APPLICATION NUMBER: US 60/396,137
PRIOR FILING DATE: 2002-07-26
PRIOR APPLICATION NUMBER: US 60/427,231
PRIOR PELING DATE: 2002-11-19
PRIOR APPLICATION NUMBER: US 60/456,496
PRIOR PELING DATE: 2003-03-24
PRIOR PELING DATE: 2003-03-24
PRIOR PELING DATE: 2003-03-06-03
NUMBER OF SEQ ID NOS: 165
SOFTWARE: Patentin version 3.2
SEQ ID NOS: 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 criarcecectaraaaracaeceeeaacearcreeraaa 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23.2%; Score 41; DB 21; L 100.0%; Pred. No. 0.00011; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (141).. (148)
OTHER INFORMATION: n may be any nucleotide
US-10-622-088-127
Bennett, Robert P.
Welch, Peter J.
Harwood, Steven
Madden, Knut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0
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2575 ccrccaccaaccaaaccaacaccrccrraardaraadarraagrradarracacacaadaga 2516
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                                                                  Gaps
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0
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                                                                                                                       137 CTTATCGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 177
                                                                                                                                                             1 CTIAICGCGCCTATAAATACAGCCCGCAACGATCTGGTAAA 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
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Query Match 23.2%; Score 41; DB 21; I
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 41; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.2%; Score 32.2; DE 61.2%; Pred. No. 0.3; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                          SQUEENCE 2338, APPLICATION US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: ISHIKAWA, JUN
APPLICANT: ISHIKAWA, JUN
APPLICANT: SHIRAWA, HIROSHI
APPLICANT: SHIRAY, VOSHIYUKI
APPLICANT: SHIRAY, VOSHIYUKI
APPLICANT: MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFREENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT PILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
NUMBER OF SEQ ID NOS: 15109
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Gaps

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APPLICAMY: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: BROSOPHILA GENES.

FILE PERERENCE: CLOOO728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT APPLICATION NUMBER: 00/167,832

PRIOR APPLICATION NUMBER: 60/160,191

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR FILING DATE: 1999-11-12

PRIOR FILING DATE: 1999-11-2

PRIOR FILING DATE: 1999-11-2

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR FILING DATE: 1999-11-2

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR FILING DATE: 1999-11-2

PRIOR PRILING DATE: 1999-12-28

PRIOR FILING DATE: 2000-01-12

PRIOR PRILING DATE: 2000-02-24

PRIOR PRILING DATE: 2000-02-24

PRIOR PRILING DATE: 2000-03-23

NUMBER OF SEQ ID NOS: 43008

SOFTWARE: FEASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 CGCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGCGACGCGCCCGTCCC 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 GACGCCAGCTTCCTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157 GGCAGCTGCGCNCCAGGTGGCTGTCCCACGCCGGTCTCCGCGCCTGCCCCGGTGCGCGGGT 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97 gécericinamicca cerrecerres references este esta de la general de la 
                                                                                                                                                                                              PEATURE:
NAME/KEX: misc feature
LOCATION: 4, 6 29, 88, 91, 146, 218, 378, 413, 482, 485, 500, 508,
LOCATION: 31, 573, 577, 585, 623, 637, 642, 651, 662, 697, 704, 724,
LOCATION: 31, 778, 835, 837, 839, 842, 852, 868, 882, 884, 885, 891,
LOCATION: 892, 899, 901
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 24; Length 921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
18.1%; Score 32; DB 24; Length 92
Best Local Similarity 51.5%; Pred. No. 0.29;
Matches 68; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match 17.4%; Score 30.8; DB 26; Best Local Similarity 55.7%; Pred. No. 0.83; Matches 59; Conservative 0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25442, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               136 GCTTATCGCGCC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Venter, J. Craig APPLICANT: et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37 TAAGATCGNGCC 26
                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-11-097-143-25442
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LENGTH: 1268
     SEQ ID NO 8561
LENGTH: 921
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Publication No. US2005027917A1

GENERAL INFORMATION:

FULL OF INVENTION:

TITLE OF INVENTION:

FILE REFERENCE: 2300-21302

CURRENT APPLICATION NUMBER: US/10/779,543

CURRENT FILING DATE: 2004-02-12

FRIOR APPLICATION NUMBER: US/10/779,555

FRIOR APPLICATION NUMBER: US/10/779,555

FRIOR APPLICATION NUMBER: 09/217,471

PRIOR APPLICATION NUMBER: 60/068,755

PRIOR APPLICATION NUMBER: 60/068,755

PRIOR APPLICATION NUMBER: 60/068,755

PRIOR APPLICATION NUMBER: 60/068,755

PRIOR PILING DATE: 1998-10-23

PRIOR FILING DATE: 1998-10-03

PRIOR FILING DATE: 1998-10-03

PRIOR FILING DATE: 1998-10-03

PRIOR FILING DATE: 1998-10-03

PRIOR FILING DATE: 1998-10-128

PRIOR FILING DATE: 1998-10-28

PRIOR FILING DATE: 1998-10-28

PRIOR FILING DATE: 1998-01-28

PRIOR PRIOR
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Remaining Frior Application data removed - See File Wrapper or PALM.
WUMBER OF SEQ ID NOS: 23767
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 9025608;
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Pred. No. 1.1;
0; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
                                                                                                                                                                                         APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SACAKI, YOSHIYUKI
APPLICANT: HATTORI, MASHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-06-02
NUMBER OF SEQ ID NOS: 15109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Streptomyces avermitilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.2%;
61.2%;
                                                                                                 ISHIKAWA, JUN
HORIKAWA, HIROSHI
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Matches 52; Conservative
OMURA, SATOSHI
IKEDA, HARUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
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                                                                                                                                                APPLICANT:
APPLICANT:
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                              17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC 76
Gaps
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) ORGANISM: DROSOPHILA US-11-097-143-38494
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557 ACAACAGCTTCCGGTGGAGGTGCCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 38434, Application US/11097143
CENDICATION NO. US20050208558A1
GENDICATION OF US20050208558A1
GENDICATION OF US20050208558A1
GENDICATION OF US20050208558A1
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR PILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 ACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGAACAGGACGC
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                                                        77 GCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    791 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 836
                                77 GCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
                                                                                                                                            Sequence 38495, Application US/11097143 Ublication No. US20050208558A1 GENERAL INFORMATION: APPLICANT: Venter, J. Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.7
Matches 59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-11-097-143-38494/c
                                                                                                               RESULT 14
US-11-097-143-38495
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1667 ACAACAGCTTCCGGTGGAGGTGCCACAAGCGGGTCCTAGTCCTTGGCGGCTCCGGTGGC 1608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1607 GTTGGCACATTGGCCATACAAATCCTCAAGTCCCAGAAAGTACAAG 1562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 GCCTCCATATCAGCCGCGCTTATCTCATGCGCGTGACCGGACACG 122
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR ALLING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-11-2
PRIOR PELING DATE: 2000-01-12
PRIOR PELING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-12
PRIOR PILING DATE: 2000-01-24
PRIOR PILING DATE: 2000-01-24
PRIOR PILING DATE: 2000-01-23
NUMBER OF SEQ ID NUMBER: 60/191,637
NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 38494
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Search completed: October 25, 2005, 06:13:38 Job time : 404.827 secs

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                                                                                                      October 24, 2005, 18:41:53 ; Search time 60.1934 Seconds (without alignments) 4811.505 Million cell updates/sec
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Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/eCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-902-540-2371
US-09-902-540-1101
US-09-252-991A-12370
US-09-252-991A-12373
US-09-252-991A-122373
US-09-126-121-22
US-09-126-121-22
US-09-126-121-22
US-09-126-121-22
US-09-126-121-22
US-09-126-121-23
US-09-126-121-23
US-09-902-540-16-13983
US-09-902-540-1717
US-09-949-016-13983
US-09-9489-0398-2740
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US-09-489-039A-2763
US-09-949-016-12134
US-09-902-540-6433
US-09-252-991A-14837
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                                                                                                                                                                                                                                                                                                                 1202784 seqs, 818138359 residues
                                                                                                                                                                               US-09-896-888A-1_COPY_351_527
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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2208
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798
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Maximum DB
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US-09-252-991A-12692/C

US-09-252-991A-12692/C

Sequence 12692, Application US/09252991A

Sequence 12692, Application US/09252991A

Patent No. 6551795

GRERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINGAS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINGAS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR PELING DATE: 1999-02-18
PRIOR PELING DATE: 1999-07-18
PRIOR PELING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 12692
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                  Sequence 2474, Ap Sequence 2551, Ap Sequence 2099, Ap Sequence 3318, Ap Sequence 1110, Ap Sequence 1154, Ap Sequence 1269 Ap Sequence 1269 Ap Sequence 11, Appli Sequence 219, App Sequence 228, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15207, A
17417, A
                                                             Sequence 2099, A
Sequence 5635, A
Sequence 1963, A
Sequence 1963, A
Sequence 1110, A
Sequence 1110, A
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Patent No. 683347
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Misgand, Roger C.
APPLICANT: Misgand, Roger C.
APPLICANT: Misgand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
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                                    US-09-489-039A-5551
US-09-902-540-2099
US-09-902-540-3318
US-09-902-540-1048
US-09-902-540-11048
US-09-902-540-11104
US-09-902-540-11164
US-09-902-540-11269
US-09-902-540-1269
US-09-902-540-1269
US-09-252-991A-219
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Best Local Similarity 57.4,
Local Similarity 57.4,
Conservative
                                          1524
4194
4902
4902
9080
12865
15321
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ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12370
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Best Local Similarity
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; ORGANISM: Pseudo
US-09-252-991A-12323
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Sequence 12370, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT PILLING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
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                                                                                                                                                                                                                                                                                                         368 GCCGCCAGTTCCTCGTCTCGACCGGAGACACCTCCATCTTCCTGACGCGTGTCAACC 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Starer, Serven C.
APPLICANT: Starer, Serven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR APPLICATION NUMBER: 60/217,883
SEQ ID NOS: 16825
SEQ ID NO 1101
LENGTH: 13579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 4.3;
0; Mismatches 47; Indels 0;
                                                                                                                                                                  Score 29.8; DB 4; Length 1311; Pred. No. 2.1; 0; Mismatches 47; Indels 0
                                                                                                                                                                                                                                                                                                                                                          105 TGCGCGTGACCGGACACGAGGCGCCCGTCCCCGCTTATCGCGCCTA 149
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                                                                                                                                                                                                                                                                                                                                                                                                      428 GGAACGGGÁCATTGGÁCGCCCCGCCGGTCACGCTCTTTACCCCCA 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1101, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
                                                                                                                                                               Query Match
Best Local Similarity 55.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.2%;
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
CRGANISM: Myxococcus xanthus
US-09-902-540-1101
                                                                    TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-2371
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SEQ ID NO 12370
LENGTH: 585
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 2371
LENGTH: 1311
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TITLE OF INVENTION: MacC 3. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 12097
LENGTH: 1443
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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUMBER: US/09/252,991A

CURRENT PILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 12333
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                                                                                                                                                                                                                                                                          8 CGTGACAGGACGCCAGCTTCCTGTGTTGCTAACCGCAGCCGGACGCAACTCCTTATCGGA
                                                                                                                                                   Gaps
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              DB 4; Length 585;
                                                                                                                                            Indels
       Score 28.6; D
Pred. No. 4.3;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
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Query Match
Best Local Similarity 53.0%;
Matches 61; Conservative
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55 ACTCCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCGCTTATCTCATGCGCGTGAC 114
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Patent No. 6252051
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: Ligands and Uses Therefor TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES. 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3; Length 2091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
16.2%; Score 28.6; DE
Best Local Similarity 58.0%; Pred. No. 6.3;
Matches 69; Conservative 0; Mismatches
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CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
                                                                                                            P1084R1
                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: Human NRG3B2 (hNRGB2)
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COALGAY, Delicate L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084
TELECHMUNICATION INFORMATION:
TELEPHONE: 650/255-2066
TELEPAX: 650/352-981
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTER STICS:
LENGTH: 2091 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: COALGY, Delidre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P108
TELEPHONE: 650/255-2066
TELEPHONE: 650/255-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
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                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 1-2091
| IDENTIFICATION METHOD:
| OTHER INFORMATION:
US-08-899-437-22
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STRANDEDNESS: Single
TOPOLOGY: Linear
FEATURE:
                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
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TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 12237

LENGTH: 2085
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Patent No. 6121415
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION:
TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                           0
                                   DB 4; Length 1551;
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                             Query Match 16.2%; Score 28.6; DB 4; Length 15
Best Local Similarity 53.0%; Pred. No. 5.8;
Matches 61; Conservative 0; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.2%; Score 28.6; DB 4; Length 20
Best Local Similarity 53.0%; Pred. No. 6.3;
Matches 61; Conservative 0; Mismatches 54; Indels
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
COMPUTER: 1BM PC compatible
COMPATER: PC-DOS/MS-DOS
SOFTWARE: WinBatin (Genentech)
CURRENT APPLICATION DATA:
FILING DATE: 24-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-12237
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                                                                                                                                                                                                                                                                                                                                                                 RESULT 7
US-09-252-991A-12237
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55 ACTCCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCTCATGCGCGTGAC 114
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Patent No. 6833447
Patent No. 6831447
Patent No. 6831467
Patent No. 6831467
Patent No. 6831467
Patent No. 6831467
Patent Saldman, Barry S.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
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                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: BrDB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSES: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STREET: Colthornia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 28.6; DB 3; Length 2502;
Pred. No. 6.7;
0; Mismatches 49; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq. LOCATION: 1-2502

LOCATION: 1-2502

IDENTIFICATION METHOD:

OTHER INFORMATION:

US-09-126-121-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P1084R1D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTATION UNMBER: 36,487
REFERENCE/DOCKET UNMBER: P108
TELECOMMUNICATION INFORMATION:
TELEFONE: 650/252-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   Sequence 5, Application US/09126121
Patent No. 6252051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 58.0%;
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2502 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-902-540-1239
                                                                                                   RESULT 11
US-09-126-121-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
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                                                                                                                                                                                                                                                      55 ACTCCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCGTTATCTCATGCGCGTGAC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               55 ACTCCTTATCGGAACAGGACGCCCTCCATATCAGCCGCGCTTATCTCATGCGCGGTGAC 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                448 ACGCCCAACCGGATTAGCACTCGCCTGACCACCA-TCACGCGGGGGCCCCACTCGCTTCCC 506
                                                                                                                                                                                                                                                                                                                                                         115 CGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGG 173
                                                                                                                                                                                                                                                                                                                                                                                                            115 CGGACACGAGGCGCCCGTCCCGCTTATCGCGCCTATAAATACAGCCCGCAACGATCTGG 173
                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-899-437-5
Sequence 5, Application US/08899437
Sequence 5, Application US/08899437
Setulo 6.121415
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: Ligands and Uses Therefor TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 3
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                           1,
                                                                                                                                                   Query Match 16.2%; Score 28.6; DB 3; Length 2091; Best Local Similarity 58.0%; Pred. No. 6.3; Matches 69; Conservative 0; Mismatches 49; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 58.0%; Pred. No. 6.7;
Matches 69; Conservative 0; Mismatches 49; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Human NRG3B1(hNRG3B1)/nucleic acid seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: COLLEY, Deirdre L.
REGISTRATION NUMBER: 91084R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-2066
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
Human NRG3B2 (hNRGB2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Genentech, Inc.
1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 2502 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
                     LOCATION: 1-2091
1 IDENTIFICATION METHOD:
COTHER INFORMATION:
US-09-126-121-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1-2502
; IDENTIFICATION METHOD:
. OTHER INFORMATION:
US-08-899-437-5
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Sequence 27806, Application US/09513999C
                                 RESULT 14
JS-09-513-999C-27806
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US-09-902-540-7217
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LENGTH: 283
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: PUTH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: uS/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-0-08
PRIOR FILING DATE: 2000-00-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 CGGAACAGGACGCGCCTCCATATCAGCCGCGTTATCTCATGCGCGTGACCGGACACGA 123
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                                                                                                                                                                                                                                                                                                                                                                                                 4 TTATCGTGACAGGACGCCAGCTTCCTGTGCTAACCGCAGCCGGACGCAACTCCTTAT 63
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                                                                                                                                                                                                                                                                                        Score 28.6; DB 4; Length 25048;
Pred. No. 13;
0; Mismatches 79; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 57320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6380 GCGGCCGTCCCCCACCTCCAGAGTAAGACAG 6414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 GGCGCCCGTCCCGCTTATCGCGCCTATAAATACAG 158
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CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF EXO ID NOS: 16825
SEQ ID NO 1239
LENGTH: 25048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.09-949-016-13983/c
Sequence 13983, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)...(57320)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13983
                                                                                                                                                                                                                                                                                           16.2%;
                                                                                                                                                                                TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-1239
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 49.04
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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ORGANISM: Human
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Stater, Steven C.
APPLICANT: Miegand, Roger C.
TITLE OF INVENTION: Myxcoccus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
PATEUR NO. 6783961
GENERAL INFORMATION:
APPLICANT: Durans Milne Edwards, J.B.
APPLICANT: Durans Milne Edwards, J.B.
APPLICANT: Durans Milne Edwards, J.B.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR FILING DATE: 1999-02-26
PRIOR FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 accacacicccrasccacrrcrrarcascacassacriccaaacsacrists 60
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Best Local Similarity 54.3%; Pred. No. 9.6;
Matches 57; Conservative 0; Mismatches 48; Indels
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Pred. No. 4.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: v=a or c or g
US-09-513-999C-27806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 68.4%;
Matches 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Myxococcus xanthus US-09-902-540-7217
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                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 3668
SOFTWARE: Patent.pm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 196
OTHER INFORMATION: m=a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: k=g
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 198
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- 1657 CAGGTGACGGGCTTCGCGGGTTGCTCCAGCCCAACGCCGGAAGCCAGGGGGAGTAC 1716 90 AQ
- Search completed: October 24, 2005, 21:57:49 Job time : 63.1934 secs

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192483 Sequence 1
103664 Sequence 2
G02286 human STS S
C0513678 Sequence
C0506464 Sequence
AJ535749 Cicer ari
                                                                                                                                                                                                                                                                                                                                             PAT 27-AUG-2002
                                                                                                                                                                                                                            M10349 Cloning vec
M12465 Bacteriopha
                                                                                                                                                                                                                                                            M31883 Cloning vec
                            AX100258 Sequence
AR038286 Sequence
AR075283 Sequence
AR152695 Sequence
                                                                                        AR238535 Sequence
AX323349 Sequence
CQ504346 Sequence
AX361570 Sequence
                                                                                                                                  A15078 Lac promote
BD175852 A method
AX404725 Sequence
                   E00523 Double-stra
                                                                    158575 Sequence 41
161307 Sequence 11
                                                                                                                                                                                                                                                  AR527545 Sequence
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Grigliatti,T.A. Theilmann,D.A., Pfeifer,T.A. and Hegedus,D.D.
Insect expression vectors
Patent: JP 2001516225-A 13 25-SEP-2001;
THE UNIVERSITY OF BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.0%; Pred. No. 2e-08;
Matches 50; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OS Unidentified
PN JP 2001516225-A/13
PD 25-SEP-2001
PF 26-MAR-1998 JP 1998541010
PR 27-MAR-1997 US 60/049946,28-JAN-1998 CA
THOMAS A GRIGILATTI, DAVE A THEILMANN, THOWAS
A PFEIFER, DWAYNE D
PI HEGEBUS
PC C12N15/85, C12N5/05, C12N15/69//C12N9/22
CC Insect expression vectors
FH Key Location/Qualifiers
FT source // Organism='Unidentified'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. 50
/mol Lype="genomic DNA"
/mol Lype="genomic DNA"
                                                                                                                                                                                                                                                                                                                                               DNA
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SYNM13MP9C
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                                       AR038286
AR075283
AR152695
                                                                                                    AX323349
CQ504346
AX361570
A15078
BD175852
AX404725
                                                                                                                                                                                            CQ513678
                                                                                          AR238535
                                                                                                                                                               192483
103664
G02286
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                                                                    158575
161307
                    E00523
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BD070868
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JP 2001516225-A/13.
                                                                                                                                                                                                                                                                                                                                                                                                        unidentified
unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                 unidentified
BD070868
                              DEFINITION
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AR006095 Homo sapi
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                                                                    ; Search time 302.908 Seconds (without alignments) 7998.346 Million cell updates/sec
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, M., Beckerly, R., Boquelavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Colling, S., Collymore, A., Colangelo, M., Colling, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kan, L., Karatas, A., Klein, J., Hebnozky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McBwan, P., McGurk, A., McKernan, K., McLaughlin, J., Mellim, J., Mellim, J., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., Cobonnell, P., Peterson, K., Pollara, V., Riley, R., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Wyman, C. & Submission

Submitted (00-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Jul 13, 2000 this sequence version replaced gi:6425709.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/Repeatmasker.html
                                                                   ACULJ392 99591 bp DNA linear HTG 13-JUL-2000 HOMO sapiens chromosome 2 clone RP11-429N24 map 2, LOW-PASS SEQUENCE SAMPLING.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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sequencing reads that have not been assembled into
contigg. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
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Contact: sequence submissions@genome.wi.mit.edu
Contact: Project Information
Center project name: 1.3805
Center clone name: 429_N_24
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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COMMENT

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Lettern, B., Lintcon, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bladwin, J., Barra, M., Dender, R., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Collins, S., Collymore, B., Bladwin, J., Barra, M., Dendelan, L., Boukhgalter, B., Bladwin, J., Barra, M., Dewar, K., Demino, M., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, M., Forrest, C., Rann, L., Reards, A., Kalan, J., Morrow, J., Waylor, J., Morrow, R., Maylor, J., Morrow, J., Waylor, J., Morrow, R., Maylor, J., Morrow, J., Waylor, J., Manean, C. H., Subramanan, A., Talams, J., Testage-Thomann, M., Stojanovic, N., Subramanian, A., Talams, J., Testage, J., Tirrell, A., Vasailiew, H., Wo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zamer, J., Maneau, J., Johnson, R., Johnson, R., Machan, J., Maneau, J., Johnson, R., Machan, J., Maneau, J., Maneau
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
                                                                                                                 Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 22, clone RP11-348B6
               AC013315.3 GI:9123904
HTG; HTGS_PHASE0.
Homo sapiens (human)
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                                                             Homo sapiens
                                                                                                                                                Unpublished
               VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                    REFERENCE
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                                        g of 754 bp in length
f 100 bp
g of 822 bp in length
f 100 bp
g of 739 bp in length
                                                                                                                                                                                                                                                                               2 100 bp
9 of 738 bp in length
f 100 bp
9 of 817 bp in length
                                                                                                                                                                                         100 bp of 805 bp in length 100 bp in length g of 815 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     f 100 bp
g of 801 bp in length
f 100 bp
f 100 bp
f 100 bp
g of 842 bp in length
of 781 bp in length
100 bp
of 765 bp in length
                                                                                                                               100 bp
of 806 bp in length
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of 809 bp in length
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of 862 bp in length
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                                                                                                                                                              100 bp
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Best Local 9
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* NOTE: This record contains 124 individual

* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows Center project name: L3764 Center clone name: 348_B_6

RESULT 3 AC013315 LOCUS DEFINITION

3876 TTAATTGCGTGGCGCTGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 3923

엄

AC013315 118229 bp DNA linear HTG 24-AUG-2002 Homo sapiens chromosome 22 clone RP11-348B6 map 22, LOW-PASS SEQUENCE SAMPLING.

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overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will be preserved.
                                                                                                                                                                                                                                                                        41: contig of 822 bp in length 11: gap of 100 bp 5: contig of 822 bp in length 5: contig of 764 bp 4: gap of 100 bp
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ACU13368 211967 bp DNA linear HTG 13-JUL-2000
HOMO sapiens clone RP11-11016, LOW-PASS SEQUENCE SAMPLING.
AC013368
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HTG; HTGS PHASE0.
HOMO sapiens (human)
Homo sapiens
Eukaryota; Metacaca; Chordata; Craniata; Vertebrata; Euteleostomi;
(hammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 211967)
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Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 19, 2000 this sequence version replaced gi:8099785.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/Repeatmasker.html
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
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Homo sapiens, clone RP11-11016
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COMMENT

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Bases I to 260636)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 18, clone CTB-155C15
Unpublished
2 (bases I to 260636)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    260636 bp DNA linear HTG 24-AUG-2002
Homo sapiens chromosome 18 clone CTB-155C15 map 18, LOW-PASS
SEQUENCE SAMPLING.
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KEYWORDS
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Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Forrest, C., Funke, R., Caged, D., Haddan, J., Gardynas, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Haddan, D., Gardynas, R., Grant, G., Karates, A., Klein, J., Henton, E., Lehocky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McDaughlin, J., Meldrim, J., Mercan, R., McGwan, R., McGwan, P., McGwan, P., McGwan, C., Loonell, P., Stanger, S., McGurk, A., Naylor, J., Norman, C.H., O'Connor, T., O'Connorl, P., Stanger, S., Tritell, A., Wossiliew, H., Wo, A., Santos, R., Severy, P., Stanger, S., Tritell, A., Vassiliew, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M. Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M. Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M. Wheeler, J., Wu, X., Myman, D., Ye, W.J., Stolancy, N., Subramanian, A., Talamas, J., Research, J. Bouthagliter, B., Brown, H., Burkett, G. Sirren, S., Baldwin, J., Bastieh, V., Bedra, F., Boguslawkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Collins, S., Gollymore, A., Cooke, P., DeArellano, K., Dewar K., Collins, S., Gollymore, A., Cooke, P., DeArellano, K., Dewar K., Calmoplano, A., Castle, A., Choepel, Y., Colangelo, M., Graham, L., Karatas, A., Klein, J., Gardynas, S., Grand, P., Marquis, N., McBann, P., McCarthy, M., McBann, P., McGurk, A., Morkernan, L., Marduis, N., McBann, P., McCarthy, M., McBann, P., McCarthy, M., McBann, P., McCarthy, M., McBann, P., McGurk, A., McGardon, K., Lahor, J., Marquis, N., McHann, J., Mencus, L., Milova, T., Miranda, C., Roych, R., Morton, L., Rymond, C., Roych, R., Rogov, P., Rothman, D., Yong, M., Mardin, J., Morton, J., Norman, C.H., O'Connor, T., O'Donnell, P., Rymond, C., Rand, M., Whan, M., Washilak, H., Viell, R., Wilson, B., Warn, W., Wann, D., Yong, Yong, G., Zainoun, J., Zimmer, A. and Zody, M. Trigillo, J., Yang, Sundas, Sundas, R., And Zodo, M., Wilson, R., Tarere, F., Carlor, R., Mardin, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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1: contig of 882 bp in length
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4: gap of 100 bp
7: contig of 890 bp in length
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contig of 876 bp in length

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contig of 889 bp in length

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39205
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HTG; HTGS PHASEO.

HOMO sapiens (human)

HOM sapiens (human)

HOM sapiens (human)

HTG; HTGS PHASEO.

HOM sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

El (bases 1 to 73282)

El (bases 1 to 73282)

Unpublished

Unpublished

Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Balram,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M., Balram,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Doyle,M., Barram,B., Deartlano,K., Dowars,Y., Dominio,M., Donelan,L., Doyle,M., Formeria,P., FitzHugh,M., Porrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Johnson,R., Jones,C., Kannt,L., Karatas,A., Klein,J., Lieu,C., Locke,K., Macdonald,P., Marquis,N., McEwaghlin,J., Neldrim,J., Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., ACC10800 73282 bp DNA linear HTG 23-SEP-1999 Homo sapiens clone 1_E_17, LOW-PASS SEQUENCE SAMPLING. ACC10800 Gaps 128125 TTAATTGTGTTGCCCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 128172 . 0 DB 2; Length 260636; 3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG Score 36.8; DB 2; Decelor No. 0.0032; 7; Indels 100 bp in length [100 bp in le 100 bp 1 of 876 bp in length 1 100 bp 1 of 875 bp in length 100 bp 100 876 bp in length 100 bp 100 bp 100 bp 100 bp 100 bp of 880 bp in length 100 bp of 871 bp in length gap of 100 bp contig of 874 bp in length gap of 100 bp contig of 870 bp in length bp in length 0; Mismatches gap of contig cap of contig c contig gap of contig gap of contig gap of contig contig gap of contig gap of contig contig gap of contig contig gap of gap of contig contig gap of contig contig contig gap of AC010800.1 GI:5919335 57663: 57763: 58633: 73.6%; 85.4%; 42137: 43012: 43112: 43980: 44080: 44959: 45059: 47017: 47994: 49944: 50826: 50926: 51806: 51906: 52777: 52877: 53760: 53860: 54727: 54827: 55699: 55799: 45943: 48970: 41; Conservative Query Match Best Local Similarity 40190 441062 42038 42038 43013 43013 43013 44308 44408 RESULT 6
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|--|---|--|--|---|-------------------------------|---|--------|----------------------------|--------|-------|--------|--------|--------|--------|--------|--------|--------|---|---------|---|---|-------|--------------|---|---|-------------------|---------|-------------------|---|-------------------|------------------|
| <pre>Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X., Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.</pre> Direct Submission | 19) Whitehead Institute/MIT Center for Genome Street, Cambridge, MA 02141, USA Itified using RepeatMasker: Smit, A.F.A. & | hington.edu/RM/RepeatMasker.html. contains 86 individual at have not been assembled into | are used to separate the reads itchy appear is completely commons of a completely com | afortary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that | ed, the accession number will | contig of 859 bp in length gap of unknown length | of 836 | contig of 851 bp in length | of 852 | | | | | | | | | gap of unknown length contig of 977 be in length | | gap of unknown length contig of 842 bp in length | gap of unknown length contig of 859 bp in length | | | gap of unknown length contig of 890 bp in length | gap of unknown length contig of 837 bp in length | unknowr of 988 | | unknown of 856 | gap of unknown length contig of 841 bp in length | unknown of 837 | unknow of 817 |
| Pollara, In,N., St Firrell,A W.J., Zi | SEP-199 Charles were iden | nome.was record c reads th | ns of N ler in wh | LOW-pass 3 clones (ationshi 5 should Tuenced t | is updated, | 859: | 1695: | 2546: | 3398: | 4263: | 5163: | 6030: | 6901: | 7717: | 8565: | 9412: | | | | - | | | 15489: | 16379: | 17216: | 18204: | 19021: | | | | •• |
| Peterson, k., Stange-Thomar Tesfaye, S., 1 Wyman, D., Ye, Direct Submis | Submitted (22 Research, 32(All repeats v | http://ftp.ge * NOTE: This * sequencing | * contigs. Ru * and the orc | * identifying * overlap rel * However, it * will be sec | * the record i | | * 860 | * 1696 * | * 2547 | 3399 | * 4264 | * 5164 | * 6031 | * 6902 | * 7718 | * 8566 | * 9413 | * 10267 | * 11244 | 12099 | * 12941 | 13800 | * * 14671 | * * 15490 | * 16380 | * 17217 | * 18205 | * * 19022 | * 19878 | * 20719 | * 21556 |
| TITLE | JOURNAL | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

g of 855 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC073998 217141 bp DNA linear HTG 30-SEP-2000
Homo sapiens clone RP11-337M23, LOW-PASS SEQUENCE SAMPLING.
AC073998
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-337M23
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Pred. No. 0.0053;
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gap of unknown length
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unknown length
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Homo sapiens (human)
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ORGANISM
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AUTHORS
TITLE
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AUTHORS
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AC073998
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Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vasiliev, H., Viel, R., Vion, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Ymor, A., and Zody, M., Zainoun, J., Zainoun, J., Submission
Submitsed (19-JUL-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Sep 30, 2000 this sequence version replaced gi:9838018.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This record contains 270 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                   Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: Project Information
Center project name: 1.7934
Center clone name: 337_M_23
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G39061 604 bp DNA linear STS 01-FEB-2001 Z11905 Zebrafish AB Danio rerio STS genomic, sequence tagged site. G39061.1 GI:3358270
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( Characa; Lo 60), Christi, J., Sim, C., Yamada, E., Kaplan, S., Jackson, D., de Sauvage, F., Jacob, H. and Fishman, M.C.

Zebrafish genetic map with 2000 microsatellite markers denomics 58 (3), 219-232 (1999)

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Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Email: fishmandmgh.cvrc.harvard.edu
http://cabrafish.mgh.harvard.edu
primer A: CACCGAGCTTCACTGACGTA
Primer B: ATACACACCCAAGCCGACAT
STS size: 112
Presoak: 94 degrees C for 5.0 minutes
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58 degrees C for 1.0 m:
27 degrees C for 1.5 m:
27 mJ Research PTC-100
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Pred. No. 0.0054;
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Best Local Similarity 83.7%;
Matches 41; Conservative
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Thermal Cycler: M
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A61P1/16,A61P3/10,A61P5/00,A61P7/02,A61P7/04,A61P7/06,A61P7/08, PC
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Pred. No. 0.0067;
0; Mismatches 8
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http://zebrafish.mgh.harvard.edu
Primer A: CACATGTGCACCGGACTCTA
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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PC A61P13/02/
PC A61P25/00/A61P25/
PC A61P27/06/
PC A61P29/00/A61P29/
PC A61P33/00/A61P35/
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Best Local Similarity 83.3%;
Matches 40; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phage; Genomic DNA from a single adult Zebrafish of AB strain was digested with Alu1, Cac81, HasII, NIAVI, or RsaI. Fragments in the range of 250-500 bp were gel purified and a BstX1 linker was added. The fragments were cloned into a modified MI3mpl9 vector and transformed into E. Coli DHSalpha. Microsatellite sequences were screened with labeled d(CA)15 and d(GT)15 oligonucleotide
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18-JAN-2000 JP 2000594904
19-JAN-1999 US 60/116330
CRAIG A ROSEN, STEVEN M RUBEN, REINHARD BENER, PAUL E YOUNG, JIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (2007) (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                        Primers are available from Research Genetics Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.resgen.com.phone: 800-533-4363).
Location/Qualifiers
                                                                                                                                                                                         1.5 mM
50 mM
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8.3
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dNTPs: each 200 uM
Tag Polymerase: 0.034 units/ul
Total Vol: 10 ul
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dev_stage="Adult"
lab_host="DH5alphaF'IQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Danio rerio"
/mol_type="genomic DNA"
/strain="AB"
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JP 2002534972-A/36
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JP 2002534972-A/36.
Homo sapiens (human)
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KCl:
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Local 40; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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VERSION
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C12P21/02, C12Q1/02, C12Q1/02, C12Q1/02, C12Q1/02, C12Q1/02, C12Q1/02, C12Q1/02, C12Q1/03, C12Q1
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                                                                                                                                                                                                  AGIP25/00, AGIP25/14, AGIP25/16, AGIP25/28, AGIP25/30, AGIP27/02, AGIP27/06, AGIP27/06, AGIP29/00, AGIP29/00, AGIP33/00, AGIP31/00, AGIP35/00, AGIP35/00,
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1 (bases 1 to 826)
Shimoda,N., Knapik,E.W., Ziniti,J., Sim,C., Yamada,E., Kaplan,S., Zackson,D., de Sauvage,F., Jacob,H. and Fishman,M.C.
Zebrafish geneic map with 2000 microsatellite markers
Genomics 58 (3), 219-212 (1999)
                                                                                          .../ 00, marris/ 02,
AGIP13/12, AGIP15/00, AGIP17/02, AGIP17/06, AGIP19/02, AGIP21/00,
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Z7956 Zebrafish AB Danio rerio STS genomic, sequence tagged site.
G40613
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Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Pax: 6177265806
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A61P9/06, A61P9/08, A61P9/10, A61P9/12, A61P9/14, A61P11/00
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/Glone lib="zebrafish AB"
/dev stage="Adult"
/lab_host="DH5alphaF'IQ"
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/note="Vectors: mi3MP19 with added BBtXI site; V-type:
Phage; Genomic DNA from a single adult Zebrafish of AB
strain was digested with Alul, Cac81, HaeIII, NlaVI, or
RsaI. Fragments in the range of 250-500 bp were gel
purified and a BstX1 linker was added. The fragments were
cloned into a modified Mi3mp19 vector and transformed
into B. COll DH5alpha. Microsatelllite sequences were
screened with labeled d(CA)15 and d(GT)15 oligonucleotide
                                                                                            Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
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Zebrafish genetic map with 2000 microsatellite markers Genomics 58 (3), 219-232 (1999) 99303552
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                                                                                                                                                                                                                                                                                                             94 degrees C for 5.0 minutes 94 degrees C for 1.0 minute 58 degrees C for 1.0 minute 72 degrees C for 1.5 minute 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.resgen.com_phone: 800-533-4363)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1.5 mM
50 mM
10 mM
8.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                10 ng
each 375 nM
each 200 uM
0.034 units/ul
10 ul
                                                                                                                                                                                       Fax: "17/22012 (18) Heben Tearner (19) Hetp://zebrafish.mgh.harvard.edu Primer A: TCAATCTCTCAAACTCCGCA Primer B: CGCTTTATAGGGCTGCAGAG STS size: 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tris-HCl:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MgCL2:
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Taq Polymerase:
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Polymerization:
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120. .139
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Best Local Similarity 83.3%
                                                                                                                                                                                                                                                                                                                                     Denaturation:
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primer_bind
ORIGIN
  TITLE
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                                                                              COMMENT
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/note="Vector: mi3MP19 with added BstXI site; V-type:
Phage; Genomic DNA from a single adult Zebrafish of AB
strain was digested with Alul, Cac81, HaeIII, NIAVI, or
Rsal. Fragments in the range of 250-500 bp were gel
purified and a BstXI linker was added. The fragments were
cloned into a modified Mi3mp19 vector and transformed
into E. Coli pHSalpha. Microsatelllite sequences were
screened with labeled d(CA)15 and d(GT)15 oligonucleotide
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1 (bases I to 979)
Shimoda,N., Knapik,E.W., Ziniti,J., Sim,C., Yamada,E., Kaplan,S., Jackson,D., de Sauvage,F., Jacob,H. and Fishman,M.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Pred. No. 0.0068;
0; Mismatches 8; Indels 0
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                                                        94 degrees C for 5.0 minutes
94 degrees C for 1.0 minute
58 degrees C for 1.0 minute
72 degrees C for 1.5 minute
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10 mM
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each 200 uM
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/mol_type="genomic DNA"
/strain="AB"
Primer B: TCTCTCCCCTGGACATCATC
STS size: 142
PCR Profile:
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/map="LG 16"
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                    HTG 13-JUL-2000
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 76295)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-165P21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
ACULISA2 Innear HTG 13-JUN HOMO Sapiens Chromosome 15 clone RP11-165P21 map 15, LOW-PASS SEQUENCE SAMPLING.
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* sequencing reads that have not been assembled into
contiggs. Runs of N are used to separate the reads

* and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-firth and allows
overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
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contig of 783 bp in length
gap of 100 bp
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Center clone name: 165_P_21
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COMMENT

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Gaps

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Mammaliar Eucheria; Frimaces; Catarrinii; Hominicae; Homo.

Mammaliar Eucheria; Frimaces; Catarrinii; Hominicae; Homo.

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Unpublished

Diarren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Bairren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

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Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Hotton, L.,

Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., Langergue, K., Lehoczky, J., Levine, R.,

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Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A.,

Travers, M., Trigillo, J., Vassillev, H., Vael, R., Vo, A., Wilson, B.,

Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and

Sody, M.,

Direct Submission
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
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AC023384.2 GI:9144035
HTG; HTGS PHASE0.
Homo sapiens (human)
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 11 clone RP11-589112 map 11, LOW-PASS
SEQUENCE SAMPLING.
                                                                                Genes, compositions, kits, and method for identification, assessment, prevention, and therapy of ovarian cancer Patent: WO 0170979-A 13142 27-SEP-2001; Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
1. 586
/organism="Homo sapiens"
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                                                                                                                                                                                                                   /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                  Lee, J. and Lillie, J.
                                                                                                                                                                                      source
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Matches

KEYWORDS SOURCE ORGANISM

DEFINITION ACCESSION

LOCUS

VERSION

RESULT 13 CQ406071

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* NOTE: This record contains 88 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved. Contact: sequence submissions@genome.wi.mit.edu ------ Project Information Center project name: L5114 Center clone name: 589_I_12 4: contig of 724 bp in length
3: contig of 749 bp in length
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Homo sapiens clone RP11-1J15, LOW-PASS SEQUENCE SAMPLING.
AC016798
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Whitehead Institute/ MIT Center for Genome Research
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sequencing reads that have not been assembled into
contigs. Runs of N are used to separate the reads
and the order in which they appear is completely
arbitrary. Low-pass sequence sampling is useful for
identifying clones that may be gene-rich and allows
overlap relationships among clones to be deduced.
However, it should not be assumed that this clone
will be sequenced to completion. In the event that
the record is updated, the accession number will
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contig of 772 bp in length
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gap of 100 bp
contig of 744 bp in length
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contig of 748 bp in length
contig of 748 bp in length
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens, clone RP11-1J15
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Web site: http://www-seq.wi.mit.edu
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HTG; HTGS_PHASE0.
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Gaps . 0 Length 95127; 9; Indels Query Match 71.2%; Score 35.6; DB 2; Best Local Similarity 82.0%; Pred. No. 0.0091; Matches 41; Conservative 0; Mismatches 9; ò

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Search completed: October 24, 2005, 20:18:17 Job time : 311.908 secs

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Anopheles gambiae GSS T7 end of clone 23P13 of library NotreDamel from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                   BQ907919 Q002012 CBM419897 R020C12 CGB86556 H010A15w AGG60720 Pan trog1 AGG114861 Pan trog1 AJ51743 Arabidops CF569104 79125 5 UB1937595 Gd94b01.y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                           B30742 HS-1003-A1-
BF703023 MI-P-E5-a
                                                                                                                                                                                                                                         AG109195 Pan trogl
AG045821 Pan trogl
CL096240 ISB1-27L3
                                                                                                                                                                                                                                                                                     AQ041632 CIT-HSP-2
CC961712 BQIDY76TF
                          AU069599
BP874955
BJ671717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web: www.genoscope.cns.fr)

2 (bases 1 to 412)

Roth,C.W., Brey,P.T., Ke,Z. and Collins,F.H.

Direct Submission
Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.

Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea;
                                                        BJ671717 E
BQ907999 C
BM419897 E
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Pred. No. 0.00023;
0; Mismatches 6;
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/ organism="Anopheles gambiae"
/ organism="Penomic DNA"
/ strain="PEST"
/ db_xref="taxon:7165"
/ clone="23P13"
/ clone lib="NotreDamel"
                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                  ATH517143
                                                                                                    CB865576
AG060720
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AG134861
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AL610451.1 GI:15916636
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Best Local Similarity 87.5%;
Matches 42; Conservative 0
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1 (bases 1 to 412)
 Genoscope.
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                                                                                                    ; Search time 360.936 Seconds (without alignments) 5273.001 Million cell updates/sec
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               GenCore version
Copyright (c) 1993 - 2005
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2364M4"
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Homo sapiens
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Unpublished (1998)
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Venter, J.C.

Use of a random human BAC End Sequence Database for Sequence-Ready
Map Building
Map Building
Dupublished (1998)

Other GSSs: CIT-HSP-2358M2.TR
Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Emai: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
ttp://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13.21
Class: BAC ends.
                                                                                                                        AQ080570 125 bp DNA linear GSS 20-AUG-1998 CIT-HSP-2358MZ.TF CIT-HSP Homo sapiens genomic clone 2358M2,
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
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1 (Dases 1 to 174)

Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, B., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random human BAC Bnd Sequence Database for Sequence-Ready
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1 Similarity 85.4%; Pred. No. 0.00082;
41; Conservative 0; Mismatches 7; Indels
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/db_xref="taxon:9606"
/clone="2358M2"
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Contact: Mark Adams
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
710 Institute for Genomic Research
711 Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
713 Medical Center Dr., Rockville, MD 20850, USA
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Fax: 301 838 0208
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Was Building
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Unpublished (1998)
Unpublished (1998)

Department of Eukaryotic Genomics
The Institute for Genomic Research
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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1 (bases 1 to 177)

Adams,M.D., Rounsley,S.D., Zhao,S., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.
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Seg primer: M13-21
Class: BAC ends.
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/mol type="genomic DNA"
/mol type="genomic DNA"
/mol xref="taxon:9606"
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/sex="Male"
/cll_type="Sperm"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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41;

Matches

DEFINITION

RESULT 5 AQ076114 ACCESSION VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

FEATURES

Query Match

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http://genome.rnet.missouri.edu/Swine/Methods.html.
Library Construction (Standard Protocol): All procedures
discussed in this section have been described in detail
elsewhere (Soares et al., 1994; Bonaldo et al., 1996;
Jiang et al., 2001). Total cellular RNA from each sample
was isolated by using STAT-60 reagent (Tel-Test,
Friendswood, TX) and poly(A) + RNA was obtained by two
rounds of purification with the Oligotex mRNA isolation
kit (Qiagen) according to the manufacturer's instructions.
The oviduct libraries and the Day 3, 6 and 10 endometrium
libraries were constructed essentially as described by the
manufacturer's instructions provided with the SuperScript
Plasmid System (Invitrogen, caf. no. 18248-013). Briefly,
Img of poly(A) + RNA will be annealed at 37 degrees Celsius
with 10mg of NotI-tag-dT18 oligonucleotide
(GCTGCTGCGCCCC-tag-T18) and reverse transcribed at 37
degrees Celsius with SuperScript I (Invitrogen) reverse
transcriptase (Jiang et al., 2001). The 'tag' represents at
tissue/stage-specific ten-base sequence identifier
(http://genome.uiowa.edu/pubsoft/software.html) present in
the oligonucleotide used to prime first-estrand synthesis.
Second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis was performed with T4 DNA
polymerase in the presence of DNA ligase and RNase H.
After second strand synthesis and digested with NoI: The CDNAs will be
size selected by passage through CDNA size fractionation
columns (Invitrogen-Life technologies). The CDNAs were
mixed on an equimolant basis and ligated directionally into
the NoII and Sall sites of the pSPORTI vector
                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (5): But to 372)
Whitworth, K.M., Springer, G.K., Bivens, N.J., Ries, J.E., Woods, R.J., Spollen, W.G., Forrester, L.J., Mathialagan, N., Prather, R.S. and Green, J.A.
Large-scale Generation and Analysis of Expressed Sequence Tags from Dordine endometrium and oviduct
Unpublished (2004)
Contact: DNA Core Facility (Swine Project)
Contact: DNA Core Facility (Swine Project)
Missouri-Columbia
Molfowersity of Missouri-Columbia
Molfowersity of Missouri-Columbia, MO 65212, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Company to the University of Missouri. Genetic Source:
Company to the University of Missouri. Genetic Source:
Company to the University of Missouri. Genetic Source:
Endometrium and oviduct tissues from various stages of the
estrous cycle were collected from crossbred pigs (Sus
scrofa domestica), frozen in liquid nitrogen immediately
after collection, and stored at -80 degrees Celsius until
RNA extraction. The specific tissues collected were Day o
and Day 3 whole oviducts and Days 3, 6, 10 and 12-14
endometrium. More information regarding the methods can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev stage="Oviduct from a gilt on day 3 of the estrous cycle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: (573)884-5552
Email: porcine@rnet.missouri.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
   scrofa cDNA 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="pd3ov"
                                                          CO990192.1 GI:51349466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: (573)882-0428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found at:
                                                                                                                                   Sus scrofa (pig)
                                                                                                                                                                  Sus scrofa
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                                                                                                    EST
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                               ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                               REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ076114 311 bp DNA linear GSS 20-AUG-1998 CIT-HSP-2368K7.TF CIT-HSP Homo sapiens genomic clone 2368K7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Map Building
Unpublished (1998)
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
Contact: Mark Adams
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-SEP-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13-21
Class: BAC ends.
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Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                        /cell_rype="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell type="Sperm"
clone lib="CIT-HSP"
note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                             73.6%; Score 36.8; DB 8; Length 177; ilarity 85.4%; Pred. No. 0.00086; Conservative 0; Mismatches 7; Indels (
                                                                                                                                                                                                                                                                                                                                                                   20
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                                                                                                                                                                                                                                                                                           7; Indels
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'db_xref="taxon:9606"
'clone="2368K7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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/sex="Male"
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Best Local Similarity 85.4
Matches 41; Conservative
                                                                                                                            HindIII"
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                                                                                                                                                                                                                                                               Local Similarity
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DEFINITION

RESULT 6 CO990192 LOCUS

à

/organism="Sus scrofa" /mol_type="mRNA" /db_xref="taxon:9823"

source

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will be electroporated into DH10B bacteria. The day 12-14 endometrium library was synthesized by Dr. Bento Soares' laboratory (University of Iowa) and was cloned into the T3T7pac vector as described elsewhere (Bonaldo et al., 1996). Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality [e.g. the presence of short polyA+ tails, genomic DNA contamination (wust be <1%), ribosomal RNA clones (must be <1%), etc.] and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. Bioinformatics work was performed by GK Springer's bioinformatics group (WG Spollen, UE Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhulyan) in Computer Science and Health Management and Informatics Departments at the University of Missouri-Columbia. Clone Sportments at the University of Missouri-Columbia. Clone Resility at: porcine@rnet.missouri.edu. Citations: 1. Bonaldo MF, Lennon G, Soares MB.

Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. 2. Jiang H, Bivens NJ, Riss JG, Miltwortk MM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2001) Constructing cDNA libraries with fewer colnes that contain long poly(dA) tails.

Biotechniques 31:38-42. 3. Soares MB. MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994.

TAG_ERSDE-Oviduct gilt Di3 of estrous cycle
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UMC-p8mm2-002-g08 8mm ovarian follicle p8mm Sus scrofa cDNA 3',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.6%; Score 36.8; DB 7; Length 37
85.4%; Pred. No. 0.00098;
ive 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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Best Local Similarity
Matches 41; Conserva
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KEYWORDS
SOURCE
ORGANISM
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/cloud.
//cloud="Vector: pignor" / relating to the Monsanto Company to the University of Missouri Genetic Source: Ovarian tissue (whole ovary, dissected follicles, or corpora lutea) was collected from crossbred pigs (Sus scrofa domestica), frozen in liquid nitrogen shortly after collection, and stored at -80 degrees Celsius until RNA extraction. The tissue from several individual pigs was pooled for the purpose of RNA extraction. The specific tissues collected were fetal whole ovary; neonatal whole ovary; prepubutal whole ovary; prepubutal whole ovary; prepubutal whole ovary; small antral follicles and corpora lutea; Day 0 follicles; Day 2 corpora lutea and Day 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Library Construction (Standard Protocol): All procedures discussed in this section have been described in detail elsewhere (Scares et al., 1994; Bonaldo et al., 1996; Jiang et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 18746-013). Briefly, Img of poly(A)+ RNA will be annealed at 37 degrees Celsius with long of Not1-tag-dr18 oligonucleotide (GTGTCTGGGGCGC-tag-T18) and reverse transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcriptase (Jiang et al., 2001). The 'tag' represente a lissue(stage-specific ten-base
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mixed on an equimolar basis and ligated directionally into
the NotI and Sall sites of the pSPORT1 vector
(Invitrogen). After ligation of the inserts, the plasmids
will be electroporated into DH10B bacteria. Preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://genome.uiowa.edu/pubsoft/software.html) present ir the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNase H. After second strand synthesis, the double-stranded cDNAs was ligated to Sall adapters (Invitrogen-Life rechnologies) and digested with Notl. The cDNAs will be size selected by passage through cDNA size fractionation columns (Invitrogen-Life technologies). The cDNAs derived from each developmental stage of a particular tissue were from each developmental stage of a particular tissue were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Management and Informatics Departments at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core facility at: porcine@rnet.missouri.edu. Citations: 1. Bonaldo MF, Lennon G, Soares MB.

Normalization and Subtractor: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   follicles. More information regarding the methods can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://genome.rnet.missouri.edu/Swine/Methods.html.
stage="8mm ovarian follicle"
                                        clone_lib="p8mm"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2004)
Conteact: DNA Core Facility (Swine Project)
Conteact: DNA Core Facility (Swine Project)
Animal Science - RS Prather
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, MO 65212, USA
TT-1: (573)882-0428
Fax: (573)884-5552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: porcine@rnet.missouri.edu
POLYA=No.
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Porcine Ovary

JOURNAL

COMMENT

TITLE

FEATURES

REFERENCE AUTHORS

DEFINITION RESULT 7 CO947892

ACCESSION

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla, Butheria, Cetartiodactyla, Suina, Suidae, Sus.

1 (Dases 1 to 425)
Jiang, H., Whitworth, K.M., Bivens, N.J., Ries, J.E., Woods, R.J., Forrester, L.J., Springer, G.K., Mathialagan, N., Agca, C., Prather, R.S. and Lucy, M.C.
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Ovariant lissue (whole ovary, dissected follicles, or
corpora lutea) was collected from crossbred pigs (Sus
scrofta domestica), frozen in liquid nitrogen shortly after
collection, and stored at -80 degrees Celsius until RNA
extraction. The tissue from several individual pigs was
pooled for the purpose of RNA extraction. The specific
tissues collected were fetal whole ovary, neonatal whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Perinatal ovary"
/clone_lib="pnatal"
/note="Vector: pSport1; Funding: A grant from the Monsanto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CO954011 425 bp mRNA linear EST 09-SEP-2004 UMC-pnatal4-004-e04 Perinatal ovary pnatal Sus scrofa cDNA 3', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ovary; prepubutal whole ovary; 2, 4, 6 and 8 mm growing follicles; Day 0 follicles; Day 5 small antral follicles and corpora lutea and Day 12 corpora lutea and Day 12 follicles. More information regarding the methods can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library Construction (Standard Protocol): All procedures discussed in this section have been described in detail elsewhere (Soares et al., 1994; Bonaldo et al., 1996;
2. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Diddion BA, Mathialagan N, Prather RS. Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Blotechniques 31:38-42. 3. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994. Construction and characterization of a normalized cDNA TAG TISSUE-Bmm ovarian follicle
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http://genome.rnet.missouri.edu/Swine/Methods.html.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.6%; Score 36.8; DB 7; Length 373; 85.4%; Pred. No. 0.00098; ive 0; Mismatches 7; Indels (
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Unpublished (2004)
Contact: DNA Core Facility (Swine Project)
Contact: DNA Core Facility (Swine Project)
University of Missouri-Columbia
M616 Medical Sciences Bldg., Columbia, M0 65212, USA
Tel: (573)882-0428
                                                                                                                                                                                                                                                                                                                                                                                           8; ...
. 0.00098; ...... 7; Indels
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Email: porcine@rnet.missouri.edu
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/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
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JOURNAL COMMENT

TITLE

FEATURES

DEFINITION

LOCUS

ACCESSION VERSION KEYWORDS SOURCE

RESULT 8 CO954011

Matches

ORGANISM

REFERENCE AUTHORS

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Sequence localizations (http://genome.ulowa.edu/pubsoft/software.html) present in the oligonucleotide used to prime first-strand synthesis. Second strand synthesis was performed with T4 DNA polymerase in the presence of DNA ligase and RNAse H. After second strand synthesis, the double-stranded cDNAs was ligated to Sall adapters (Invitrogen-Life echnologies) and digested with NoLI. The CDNAs will be size selected by passage through CDNA size fractionation columns (Invitrogen-Life technologies). The CDNAs derived from each developmental stage of a particular tissue were mixed on an equimolar basis and ligated directionally into the Notl and Sall sites of the pSPORTY vector. (Invitrogen). After ligation of the inserts, the plasmids will be electroporated into DH10B bacteria. Preliminary Library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality (e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%) etc.) and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility Bioinformatics work was performed by GK Springer's bioinformatics group (WG Spollen, JE Ries, A Guillen, AA Khambati, RV Patel, CM Topinka, SB Bhuiyan) in Computer Science and Health Management and Informatics Departments a clones to clones
Using et al., 2001). Total cellular RNA from each sample was isolated by using STAT-60 reagent (Tel-Test, Friendswood, TX) and the poly(A)+ RNA was obtained by two rounds of purification with the Oligotex mRNA isolation kit (Qiagen) according to the manufacturer's instructions. The libraries were constructed essentially as described by the manufacturer's instructions provided with the SuperScript Plasmid System (Invitrogen, cat. no. 1824e-013). Briefly, 1mg of poly(A)+ RNA will be annealed at 37 degrees (GETCCTGGGGCGC-Ctag-T18) and reverse transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcribed at 37 degrees Celsius with SuperScript II (Invitrogen) reverse transcribtes (GractCTGGGCCGC-tag-T18). The 'tag' represents a tissue(Stage-specific ten-base sequence identifier
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Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996, 6:791-806.
2. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathialagan N, Prather RS, Lucy MC (2010) Constructing cDNA libraries with fewer clones that contain long poly (dA) tails. Biotechniques 31:38-42. 3. Soares MB, MF Banaldo, P Jelene, L Su, L Lawton, A Efstrantiadis. 1994.
Construction and characterization of a normalized CDNA library.
Proc. Natl. Acad Sci, 91:9228-9232.
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85.4%; Pred. No. 0.001;
ive 0; Mismatches 7; Indels
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TAG_TISSUE=Perinatal ovary
TAG_SEQ=Not found"
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Best Local Similarity
Matches 41; Conserv
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LOCUS
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Submitted (01-OCT-2001) BBMI, Institut Pasteur, 25, rue du Dr.
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JOURNAL
COMMENT
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AUTHORS
    JOURNAL
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KEYWORDS
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                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Schuch, Gale, M., Graner, A., Gustafson, D.-A., Appels, R., Bailey, P., Blake, T., Close, T., Gustafson, P., Herrmann, R.G., Holton, T., Gaquemin, J. M., Graner, P., Joudrier, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Socriells, M., Walburton, M., Ralvaraj, G., Shariflou, M., Sorrells, M., Walburton, Citte, Triticeae Expressed Sequence Tags for Species of the Triticeae Unpublished (2000)
Contact: Jacquemin JM
Centre de Recherches Agronomiques, Departement de Biotechnologie 234 chaussee de Charleroi, 5030 Gembloux BELGIUM
Tel: 32 81 61 29 35
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GBX002.C11F990602#08 ITEC GBX Wheat Root Library Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS07H85
Anopheles gambiae GSS T7 end of clone 25H23 of library NotreDamel from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="root"
/dev_stage="seedling, unstressed"
/clone_lib="ITEC GBX Wheat Root Library"
/note="Vector: pUC18; 0.3-2.0 Kbp average insert size."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.6%; Score 36.8; DB 2; Length 451; 85.4%; Pred. No. 0.001; ive 0; Mismatches 7; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: jacquemin@cragx.fgov.be
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Triticum aestivum"
                     cDNA clone GBX002.C11, mRNA sequence.
BE403103
                                                                                                            Triticum aestivum (bread wheat)
Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="GBX002.C11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/cultivar="Odeon"
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AL610727.1 GI:15916912
                                                                BE403103.1 GI:9362483
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/dD.xerE="taxon:3702"
/clone="tk6607"
/tissue_type="Whole Plant"
/tissue_type="Whole Plant"
/clone lib="Axabidopsis RT-PCR Products (CSHL)"
/note="DNA was extracted from Arabidopsis thaliana whole plant tissue, provided by members of Rob Martienssen's lab, using TRIZOL. Primers were designed in Hypothetical genes and un-annotated regions in Arabidopsis that are conserved in Brassica oleracea located in the short arm of chromosome 4. PCR products were either cloned into pCR TOPO 2.1 vector (Invitrogen) and then sequenced using -21 Ml3 forward and reverse universal primers or treated with Exonuclease 1 and Shrimp Alkaline phosphatase and sequenced using the specific primers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             591 bp mRNA linear EST 14-JUN-2004 tk66a07.b7 Arabidopsis RT-PCR Products (CSHL) Arabidopsis thaliana CO048749
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Arabidopsis thaliana
Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Roux, Paris 75015, France
This close is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
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500 Sunnyside Blvd., Plainview, NY 11797, USA
Tel: 516 422 4086
Fax: 516 422 4109
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                                                                                                                                                                                           /mol_type="genomic DNA"
/arrain="PEST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.6%; Score 36.8; DB 985.4%; Pred. No. 0.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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/clone="25H23"
/clone_lib="NotreDame1"
/note="end : T7"
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Plate: tk66 row: a column: 07
High quality sequence stop: 591.
Location/Qualifiers
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/db_xref="taxon:3702"
                                                                                                                                         Location/Qualifiers
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Woodbury Genome Center
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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R.Site 2 : SacI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (U2-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehitro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbe@ggs.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: PTB-041G18.F, genomic survey sequence.
AG055437
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Pan troglodytes DNA, clone: PTB-059B24.F, genomic survey sequence.
AG068743
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Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 641)
Rujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watenabe, H. and Sakaki, Y.
Direct Submission
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                                                                                    217 TTATTTTTGTTGCCCCCCCTTTCCAGTCGGGAAACCTGTCG 264
73.6%; Score 36.8; DB 7; Length 591; ilarity 85.4%; Pred. No. 0.0011; Conservative 0; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                     3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="PTB-059B24.F"
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R.Site 2
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Matches 41; Conserv
                  Local Similarity
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Submitted (02-MUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Ranagawa 210-0045, Japan (E-mal:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Direct Submission

Direct Submission

Direct Submission

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
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Pan troglodytes DNA, clone: PTB-135016.F, genomic survey sequence.
AG125607
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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BAC end sequences of Library PTB
Unpublished
        Taylor, T.D., Yada, T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="PTB-041G18.F"
/sex="male"
Fujiyama,A., Hattori,M., Toyoda,A.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:sis1-45-503-9111, Pax:181-45-503-9110,
Glones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
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AG118925.1 GI:16739444
GSS.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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85.4%; Pred. No. 0.0011;
tive 0; Mismatches 7; Indels (
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/clone_lib="PTB Chimpanzee Male BAC Library"
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/db_xref="taxon:9598"
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Sequencing: -21M13
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R.Site 1
R.Site 2
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R.Site 2
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                                                                                  Vector
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VERSION
KEYWORDS
SOURCE
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AG118925
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AUTHORS
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3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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Job time : 367.936 secs
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Primers AAV62497 and AAV62498 were used for the construction of the plasmid p2Z0p2J-3. The invention provides a new shuttle vector for transforming insect calls that comprises: (i) prokaryotic origin of replication; (ii) insect promoter having homology to, and capible of functioning as, an immediate early baculovirus promoter; (iii)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Grigliatti TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1997;
28-JAN-1998;
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Ad139252 Human ova
Aa877556 DNA encod
Aa869138 DNA encod
Aa877547 DNA encod
Aa877547 DNA encod
Aa877551 DNA encod
Aa877551 DNA encod
Aa609733 Novel DNA
Aa669873 DNA encod
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Breast ca
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Ade48102 Human che
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Aas89978 DNA encod
Aas92596 DNA encod
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Aas85906 DNA encod
Aas92595 DNA encod
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                                                     ; Search time 54.6144 Seconds (without alignments) 5419.578 Million cell updates/sec
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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                             4390206 seqs, 2959870667 residues
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                                                      October 24, 2005, 18:39:18;
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Maximum Match 100%
Listing first 45 summaries
                                    - nucleic search, using sw model
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ACN83021
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ADL39252
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AAS92595
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| Aaf55402 Sequence Aaf55403 Sequence | ന | Aat01221 Oligonucl | Aav62171 HSV-2 str | Abv36253 Human pro | Aak85632 Human imm | Abv45247 Human pro | Aan60799 Portion o | Aak85619 Human imm | Aak90169 Human dig | Aak89383 Human dig | Aak89976 Human dig | Aak79577 Human imm | Aak85615 Human imm | Aak85621 Human imm | | Aak85628 Human imm | Aak85633 Human imm | Aak85616 Human imm | Aak73946 Human imm | Aak69739 Human imm | Aak69742 Human imm | Aak85617 Human imm | Aak85618 Human imm |
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| AAF55402 AAF55403 | ADL18713 | AAT01221 | AAV62171 | ABV36253 | AAK85632 | ABV45247 | AAN60799 | AAK85619 | AAK90169 | AAK89383 | AAK89976 | AAK79577 | AAK85615 | AAK85621 | AAK85626 | AAK85628 | AAK85633 | AAK85616 | AAK73946 | AAK69739 | AAK69742 | AAK85617 | AAK85618 |
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| 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 | 70.4 |
| 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 | 35.2 |
| 22 | 23 | Ŋ | 25 | 56 | N | 28 | 59 | m | 31 | 32 | m | m | m | 36 | n | m | m | 4 | 4 | 42 | 43 | 44 | 45 |
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ALIGNMENTS

Expression vectors for transforming insect cells from disparate lines Op ie2; promoter; shuttle vector; transformation; melanotransferrin; immediate early baculovirus promoter; prokaryotic; transcription; bloemycin/phleomycin-type antibiotic; insect cell; transposon; ion transport peptide hormone; PCR primer; ss. useful to express heterologous DNA, e.g. to allow study of gene expression and produce commercially important proteins. Hegedus DD; Pfeifer TA, Plasmid p2ZOp2J-3 constructing primer 2. Disclosure; Page 39; 121pp; English. Theilmann DA, BP (UYBR-) UNIV BRITISH COLUMBIA 97US-0049946P. 98CA-02221819. 98WO-CA000282. AAV62498 standard; DNA; 50 (first entry) WPI; 1998-557129/47.

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prokaryotic promoter sequence, and (iv) selectable marker capable of conferring resistance to a bleomycin/phleomycin-type antibiotic under transcriptional control of (ii) and (iii), in insect and prokaryotic cells respectively. The vectors can be used to stably transform (especially insect) cells with heterologous DNA, is useful to allow study of gene expression and direct expression of heterologous gene products, such as commercially important proteins. They are especially useful to allow expression of melanotransferrins, ion transport peptide hormones or biologically active derivatives in insect cells. They enable transformation of insect cell lines from disparate species, allowing screening of lines for optimum post-translational modification of
                                                                                                                                                                                                                                                                                                                                                                  particular proteins. Shuttle vectors further comprising DNA transposable elements defining a transposon can be used to optimise heterologous
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Sequence 50 BP; 11 A; 14 C; 12 G; 13 T; 0 U; 0 Other;

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                                                                      1 ACTTAAGCTTATAGCGATGACTGCCCCCTTTCCAGTCGGGAAACCTGTCG
                                                        1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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hes 50; Conservative
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DNA encoding novel human diagnostic protein #25782. AAS89978 standard; cDNA; 16091 BP. (first entry) 13-FEB-2002 AAS89978; AAS89978/c

Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.

Homo sapiens

WO200175067-A2

11-OCT-2001.

30-MAR-2001; 2001WO-US008631.

31-MAR-2000; 2000US-00540217. 23-AUG-2000; 2000US-00649167.

(HYSE-) HYSEQ INC

Drmanac RT, Liu C,

Tang YT;

WPI; 2001-639362/73 P-PSDB; ABG25791 New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity

Claim 1; SEQ ID NO 25782; 103pp; English.

The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food

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              of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The propagate and polymediate sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and
                                                                                                                                 amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
supplement. (II) and its binding partners are useful in medical imaging
                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                              Sequence 16091 BP; 4724 A; 3867 C; 3861 G; 3639 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                   DB 5; Length 16091; 0.00011; ches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            8080 GTTTATTGCAATCATTGCCCGCTTTCCAGTCGGAAACCTGTCG 8037
                                                                                                                                                                                                                                                                                                                                                                                       7 GCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding novel human diagnostic protein #28400.
                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 28400; 103pp; English.
                                                                                                                                                                                                   electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                       Score 36,
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS92596 standard; cDNA; 20795 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                     72.0%;
Local Similarity 88.6%;
les 39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; ABG28409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAS92596;
                                                                                                                                                                                                                                                                                                       Query Match
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Matches
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AAS92596
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involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The polynucleotide sequences given in AAB25665 to AAB27708 encodes the human secreted proteins given in AAB25665 to AAB25755. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: immunosuppressive; immunostimulant; antiinflammatory; cardiant; vulnerary; antiulcer; nootropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective; antipacterial; antipacterial; anticonvulsant; antipacterial; and cytostatic. The secreted proteins and their polymucleotides can be used in gene therapy and as vaccines, chemotaxismodulators and anglogenesis- modulators. The human secreted proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; immunosuppressive; immunostimulant; nootropic; antiinformatory; cardiant; vulnerary; antiulocr; antionrulaant; antiparkinsonian; neuroprotective; antivoral; antibacterial; cytostatic; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic; antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic; cancer; immune system disorder; hyperproliferative disorder; infection; cardiovasçular disorder; hyperproliferative disorder; infection; cardiovasçular disorder; neurological disease; wound healing; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide encoding a secreted protein useful for preventing, treating or ameliorating a medical condition.
                                                                                                                                                                                                                                   Sequence 20795 BP; 4255 A; 5208 C; 5716 G; 5614 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                               72.0%; Score 36; DB 5; Length 20795; 88.6%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                              12363 GTTTATTGCAATCATTGCCGGTTTTCCAGTCGGGAAACCTGTCG 12406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein gene 27 SEQ ID NO:37.
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 394; 451pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA87692/c
ID AAA87692 standard; cDNA; 745 BP.
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Birse CE;
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ses 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB25691
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200043495-A2.
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polynucleotides can be used for diagnosing (the susceptibility to) a pathological condition by determining the presence or absence of a mutation in the polynucleotide or determining the presence or amount of expression of the protein. The polynucleotides and proteins can also be used in the treatment and diagnosis of cancer, diseases of the immune system, hyperproliferative disorders, cardiovascular disorders and neurological disease. They can also be used to promote wound healing and to fight infection, AAA87657 to AAA87665 and AAB25664 represent sequences
                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
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                                                                                                                                                                                                                                           71.6%; Score 35.8; DB 3; Length 745; 83.3%; Pred. No. 5.9e-05; ive 0; Mismatches 8; Indels C
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                                                                                                                                                                                                       Sequence 745 BP; 191 A; 214 C; 188 G; 142 T; 0 U; 10 Other;
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                                                                                                                                                                                                                                                                                                                             3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     site at seqdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                               in the exemplification of the present invention
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83.3%; Pred. No. 6e-05;
ive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Breast cancer related marker, seg id 7241.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP.
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Best Local Similarity 83.3%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                Local Similarity 83.3%;
les 40; Conservative
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                                                                                                                                                                                                                  21-AUG-1999;
17-SEP-1999;
                                                                                  Unidentified
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                                                                                                                                                                                                                                                                                                      Davis M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleid acid molecule comprising a nucleotide sequence (SI). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for detecting the presence of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN98294 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
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                                                                                                                                                                                                                                                                     Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTAATTGCGTTGCGCTNACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 616
                                    544 TTAATTGCGTNGCGCTCACTGCCCGCTTTCCAGTCGGAAACCTGTCG 591
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                 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification but may be obtained in electronic format frosite at segdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 4171; 36pp; English.
                                                                                                                                                                                                                                   Breast cancer related marker, seq id 4171.
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                                                                                                                                   BP.
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                                                                                                                                   ACN83021 standard; DNA; 869
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The specification describes new purified recombinant thermostable DNA polymerases having an amino acid substitution at E681. The new DNA polymerases have improved discrimination properties (and thus resulting in improved signal uniformity) and increased tolerance to high salt conditions. They also modulate the incorporation of terminators having a net positive or net negative charge during sequencing. The recombinant thermostable DNA polymerases are useful in many recombinant DNA techniques, e.g. nucleic acid amplification by polymerase chain reaction, self-sustained sequence replication, or high temperature DNA sequencing. The recombinant thermostable DNA polymerases are also useful in nucleasing the uniformity of dye-terminator incorporation in fluorescent dye DNA sequencing with a modified Tag DNA polymerase of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New purified recombinant thermostable DNA polymerases having amino acid substitutions at E410R or E681R, useful in recombinant DNA techniques, e.g. nucleic acid amplification or high temperature DNA sequencing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Thermostable DNA polymerase, signal uniformity, salt tolerance, nucleic acid amplification; polymerase chain reaction; pREFY2pref; self-sustained sequence replication; DNA sequencing; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nampalli S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Finn PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (AMSH ) AMERSHAM PHARMACIA BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian cancer DNA marker #13142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 7; 48pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kumar S,
                                                                                                                                                                                                                                                                                                                                                                                                                                10-AUG-2000; 2000WO-US022150.
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99US-0154739P.
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food supplement; medical imaging; diagnostic; genetic disorder;
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ID AAS77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                     The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. noncancerus) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the encoded by the markers, antibodies that selectively bind to the conclusion ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the expression levels indicates ovarian cancer. The level of expression of expression levels indicates ovarian cancer. The level of expression of polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed corresponding to the marker. The presence of grotein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed corresponding to the marker. The presence of protein or protein or protein or protein with the marker is assessed by detecting the presence of protein or protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymicleotide which and such the marker or ameals with a portion of the polymicleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the
                                                                                                                                                                                                                                                         Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 ATTTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 586 BP; 168 A; 131 C; 141 G; 146 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding novel human diagnostic protein #13360.
                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 13142; 106pp; English.
                                                                                                                                       (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS77556 standard; cDNA; 1637 BP.
                                     2000US-0211940P.
2000US-0216820P.
2000US-0191031P
                    20,00US-0207124P
                                                                            2000US-0220661P.
2000US-0257672P.
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Best Local Similarity
                                                                                                                                                                                                                   WPI; 2001-611502/70.
                                                                                                                                                                              Lillie J;
                                                        07-JUL-2000; 2
25-JUL-2000; 2
21-DEC-2000; 2
                                       .5-JUN-2000;
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                                                                                                                                                                              Lee J,
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PGF) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). (He polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I is useful in gene therapy techniques to restore normal cutivity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in the responsible for genetic disorders or other traits to assess buddiversity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                359 AATTAATTGCGTTGGCCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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AAS77545 standard; cDNA; 1695
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                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; ABG13369
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                                                                          Homo sapiens
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reaction (PCR) primers, oligomers, and for chromosome and gene mapping reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II) The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal cativity of (II) or the treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of stees expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in dispandances, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of date and products dependent on DNA and in the cation of mutations and to produce other types of date and products dependent on DNA and in the cation of mutations and to produce other types of date and products dependent on DNA and in the cation of mutations and to produce other types of date and products dependent on DNA and in the cation of mutations and to produce other types of date and products dependent on DNA and in the cation of mutations and to produce other types of date and products dependent on DNA and in the cation of mutations and the cation of mutatio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                  31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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Best Local Similarity 82.0
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-639362/73
                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; ABG04951
   WO200175067-A2.
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                                                                 11-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 13349; 103pp; English.
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                                                                                                                                                                                                                                                            2000US-00540217.
2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT;
                                                                                                                                                                                           30-MAR-2001; 2001WO-US008631
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82.0%;
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Best Local Similarity
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                                                              WO200175067-A2
Homo sapiens
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                                                                                                                                                                                                                                                                31-MAR-2000;
                                                                                                                                                                                                                                                                                               23-AUG-2000;
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                                          Length 1942;
                                                                                                                                                   1 ACTTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
Sequence 1942 BP; 516 A; 524 C; 495 G; 407 T; 0 U; 0 Other;
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding novel human diagnostic protein #13351.
                                             Score 35.6; DB 5;
Pred. No. 9.1e-05;
0; Mismatches 9;
                                                                                                0; Mismatches
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Homo sapiens

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RESULT 11 AAS69138/ us-09-896-888a-10.rng

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The invention relates to isolated polynucleotide (1) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chomosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed centuity of (II) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful in sisue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations diagnostics. Forensics of disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences have applicated on DNA and amino acid sequences have seven therefore the polymeral of the products dependent on DNA and amino acid sequences have seven therefore the polymeral of the products dependent on DNA and amino acid sequences have seven therefore the polymeral of the products dependent on DNA and amino acid sequences have applications in the polymeral of the products dependent on DNA and amino acid sequences have a publications in the polymeral of the products dependent on DNA and amino acid sequences have a publications in the polymeral of the products dependent on DNA and the polymeral of the products dependent on DNA and the polymeral of the products dependent on DNA and the polymeral of the products dependent on DNA and the polymeral of the products dependent on DNA and the polymeral of the products dependent on DNA and the polymeral of the products dependent on DNA and the polymeral of the products dependent on DNA and the polymeral of the polymeral of the produc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #13365.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71.2%; Score 35.6; DB 5; 82.0%; Pred. No. 9.7e-05; iive 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 23327; 103pp; English.
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ID AAS77561 standard; cDNA; 2710
                                                                                                                                                                                                                             Tang YT;
      30-MAR-2001; 2001WO-US008631.
                                                               31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.2%; Score 35.6; DB 5; Length 2:
82.0%; Pred. No. 9.6e-05;
iive 0; Mismatches 9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 13351; 103pp; English.
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ID AAS87523 standard; cDNA; 2424 BP.
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                                                                                                                        31-MAR-2000; 2000US-00540217, 23-AUG-2000; 2000US-00649167,
                                                               30-MAR-2001; 2001WO-US008631
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Best Local Similarity 82.0
Matches 41; Conservative
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chromosome marker; genetic disorder; contig; ds.
                                                                                                                                                                       diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in
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                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 13365; 103pp; English.
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                                                                            Tang YT;
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11-DEC-2001; 2001US-0339453P.
31-MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41; Conservative
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                                                                            Liu C,
                                                                                                         WPI; 2001-639362/73
                                             (HYSE-) HYSEQ INC
                                                                                                                           P-PSDB; ABG13374
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                                                                                                                                                                                                      biodiversity.
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Best Local S
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The invention comprises the amino acid and coding sequences of novel proteins. The DNA and procein sequences of the invention are useful as: markers for tissues in which the corresponding protein is preferentially expressed; as molecular weight markers on gels; as chromosome markers or tags; to identify chromosomes or to map related gene positions; and to genetic disorders. The present DNA sequences in patients to identify potential exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides, useful for expressing recombinant proteins for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding protein is preferentially expressed.
                                                                                                                                                                                                                                                                                                          Wang J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                   Asundi V, Goodrich RW, Ren F, Zhang
Xue AJ, Wehrman T, Weng G, Zhou P,
ng D, Chen R, Xu C, Boyle BJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 2277; 1177pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: October 24, 2005, 18:58:10 Job time : 59.6144 secs
14-MAR-2002; 2002US-0365091P.
14-MAR-2002; 2002US-0365884P.
12-ARR-2002; 2002US-0372381P.
12-ARR-2002; 2002US-0372615P.
22-ARR-2002; 2002US-00128558.
24-APR-2002; 2002US-0376045P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-569235/53.
                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                    Ma Y, Wang D,
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Sequence 4171, Ap Sequence 80752, A Sequence 2086, Ap Sequence 2087, Ap Sequence 2087, Ap Sequence 13360, A Sequence 13367, Ap Sequence 2337, Ap Sequence 2336, Ap Sequence 2470, App Sequence 347, App Sequence 286, App Sequence 286, App Sequence 114, App Sequence 114, App Sequence 114, App Sequence 114, App Sequence 11, Appl Sequence 1, Appli Sequence 8, Appli

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    FEATURE:

        OTHER INFORMATION: Description of Artificial Sequence: Primer

        US-09-896-8884-10

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100.0%; Score 50; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.4e-11;
Matches 50; Conservative 0; Mismatches 0; Indels
5 US-10-198-846-4171
US-09-814-35-13142
US-09-814-35-13142
US-09-814-35-13142
US-09-814-35-13142
US-00-27-632-2086
US-10-027-632-2086
US-10-027-632-2086
US-10-027-632-2086
US-10-027-632-2087
US-10-450-763-13365
US-10-205-463-347
US-10-313-872-36
US-10-205-428-959
US-10-205-428-959
US-10-205-637-8
US-10-205-637-8
US-10-205-637-8
US-10-319-2277-44
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US-10-319-2277-44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-896-888A-10; Sequence 10, Application US/09896888A; Patent No. US20020116723A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
  SEQ ID NO 10
LENGTH: 50
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Sequence 25782, A
Sequence 28400, A
Sequence 37, Appl
Sequence 7241, Ap
                                                                                                                                                          // Search time 102.023 Seconds
(without alignments)
4044.488 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO7_NEW PUB.seq:*
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29: /cgn2_
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                          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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4 US-10-450-763-25782
4 US-10-450-763-28400
1 US-09-985-153-37
5 US-10-198-846-7241
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                      9772363 seqs, 4126298632 residues
                                                                                                                                                               October 24, 2005, 20:18:24;
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 - nucleic search, using sw model
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Match Length DB ID
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seq length: 200000000
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35.8
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Maximum DB :
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                                                        Length 20795;
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                                                                                                                                            7 GCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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                                                                                                                                                                                                                                                                            Sequence 37, Application US/0985153
Publication No. US20040181047A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 33 Human Secreted Proteins
FILE REFRENCE: P2036P1
CURRENT APPLICATION UNMER: US/09/985,153
CURRENT FILING DATE: 2001-11-01
PRIOR PILING DATE: 2000-07-17
PRIOR PELING DATE: 2000-07-17
PRIOR PELING DATE: 2000-01-18
PRIOR FILING DATE: 2000-01-18
PRIOR FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 745
                                                          72.0%; Score 36; DB 24;
88.6%; Pred. No. 8.2e-05;
                                                                                                   0; Mismatches
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; OTHER INFORMATION: n equals a,t,g, or c
US-09-985-153-37
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OTHER INFORMATION: n equals a,t,g, or
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LOCATION: (3)
OTHER INFORMATION: n equals a,t,g,
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LOCATION: (93)
OTHER INFORMATION: n equals a,t,g,
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OTHER INFORMATION: n = a,t,c or
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OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
                                                                             Best Local Similarity 88.6
Matches 39; Conservative
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                   US-10-450-763-28400
                                                                                                                                                                                                                                                                     US-09-985-153-37/c
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OTHER INFORMATION: 100% homologous to Cloning vector pBACe3.6
OTHER INFORMATION: levansucrase, accession number U80929, Smith-Waterman Score=110.
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                     ACTTAAAGCTTATAAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.0%; Score 36; DB 24; Length 16091; 88.6%; Pred. No. 7.8e-05; tive 0; Mismatches 5; Indels 0
                                                                                                                             Sequence 25782, 267.

Sequence 25782, 3pplication US/10450763

Publication No. US20050196754A1

GENERAL INFORMATION:

APPLICANT: Hyseq. IN WOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 790CIP3/US

CURRENT APPLICATION NUMBER: US/10/450, 763

CURRENT FILING DATE: 2003-06-11

PRIOR PELING DATE: 2001-03-30

PRIOR PILING DATE: 2001-03-30

PRIOR FILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-03-31

PRIOR PILING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8080 GTTTATTGCAATCATTGCCCGCTTTCCAGTCGGGAAACCTGTCG 8037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REPERENCE: 790C193/US

CURRENT APPLICATION NUMBER: US/10/450,763

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: OS/540,217

PRIOR APPLICATION NUMBER: 09/540,217

PRIOR PLICATION NUMBER: 09/540,167

PRIOR PLICATION NUMBER: 09/649,167

PRIOR APPLICATION NUMBER: 09/649,167

PRIOR PLING DATE: 2000-08-23

NUMBER OF SEQ ID NOS: 60736

SEQ ID NO 28400

LENGTH: 20795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 GCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-450-763-28400

'Sequence 28400, Application US/10450763

; Publication No. US20050196754A1

; GENERAL INFORMATION:
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Best Local Similarity 88.6*
...has 39; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SIMILAR
LOCATION: (961)...
                                                                                                                       US-10-450-763-25782/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 25782
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569 TTAATTGCGTTGCGCTAACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 616
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                                                                                                              US-10-437-963-80752/c
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                                                                        GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Lillie, James
APPLICANT: M. Yongyao
APPLICANT: W. Yongyao
APPLICANT: Warg, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TITLE OF INVENTION: THERAPY OF BREAST CANCER
FILL REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: 0502-07-18
CURRENT PILLING DATE: 2002-07-18
PRIOR PLING DATE: 2001-07-18
PRIOR FILING DATE: 2001-07-18
SPRIOR FILING DATE: 2001-07-18
SOFTWARE FARENCE: FARENCE: Andows Version 4.0
SEQ ID NO 7241
LENGTH: 791
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
; LOCATION: 282, 300, 554, 592, 650, 707, 720, 728, 755, 767, 775, 791
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-7241
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; NAME/KEY: misc_feature

; LOCATION: 2, 3, 4, 6, 9, 10, 11, 531, 585, 667, 691, 696, 732, 742,

; LOCATION: 763, 764, 780, 816, 841, 856

; OTHER INFORMATION: n = A,T,C or G

US-10-198-846-4171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 71.6%; Score 35.8; DB 15; Length 791; Best Local Similarity 83.3%; Pred. No. 5.4e-05; Matches 40; Conservative 0; Mismatches 8; Indels 0
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              US-10-198-846-7241
; Sequence 7241, Application US/10198846
; Publication No. US20030099974A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Gaps

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3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50

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APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yould, Xihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION VUMBER: US/10/437,963
CURRENT FILING DATE: 2003-65-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 80752
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GENERAL INFORMATION:
APPLICANT: Thompson, Pamela
APPLICANT: Lillie, John
APPLICANT: Lillie, John
APPLICANT: Lillie, James
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
FILE REFERENCE: MRI-006B
CURRENT APPLICATION NUMBER: US/09/814,353
CURRENT FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: US 60/191,031
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PILING DATE: 2000-05-25
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/211,940
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-25
PRIOR PELING DATE: 2000-07-27
PRIOR PELING DATE: 2000-07-07
PRIOR PELING DATE: 2000-07-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 71.2%; Score 35.6; DB 20; Best Local Similarity 82.0%; Pred. No. 5.9e-05; Matches 41; Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT4530_80346C.1
US-10-437-963-80752
Sequence 80752, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 13142, Application US/09814353 Publication No. US20030165831A1
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; ORGANISM: HOMO E
US-09-814-353-13142
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RESULT 11
US-10-027-632-2086/c
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ORGANISM: Human
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ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 2087
LENGTH: 865
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| Sequence 2086, Application US/10027632
| Publication No. US20020198371A1
| GENERAL INFORMATION:
| APPLICANT: Wang, David G. |
| TITLE OF INVENTION: Identification and Mapping of Single Nucleotide |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| TITLE OF INVENTION: Polymorphisms in the Human Genome |
| TITLE OF INVENTION: DOLYMORPHISMS in the Human Genome |
| FILE REFERENCE: 108827.129 |
| CURRENT APPLICATION NUMBER: US 60/198,676 |
| PRIOR FILING DATE: 2000-04-20 |
| PRIOR PELICATION NUMBER: US 60/198,676 |
| PRIOR PELICATION NUMBER: US 60/195,218 |
| PRIOR FILING DATE: 2000-03-29 |
| PRIOR FILING DATE: 2000-03-29 |
| PRIOR FILING DATE: 1999-11-23 |
| PRIOR FILING DATE: 1999-09-28 |
| PRIOR FILING DATE: 1999-09-80 |
| PRIOR FILING DATE: 1999-09-80 |
| PRIOR FILING DATE: 1999-08-09 |
| SOFTWARE: FastESQ for Windows Version 4.0
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                                                                                               Gaps
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                                                                                                                                                                                                                                              516 ATTTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 AATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 231
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    Score 35.6; DB 10; Length 586;
Pred. No. 6.3e-05;
0; Mismatches 9; Indels 0
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US-10-027-632-2086
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Matches 41: Conscrete
ch 71.2%;
l Similarity 82.0%;
41; Conservative
Query Match
Best Local Similarity
Matches 41; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                           -10-027-632-2086/c
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ORGANISM: Human
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LENGTH: 865
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JUNEARLY LINCANTALION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR APPLICATION NUMBER: US 60/166,368
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-08-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 71.2%; Score 35.6; DB 14;
Best Local Similarity 82.0%; Pred. No. 6.7e-05;
Matches 41; Conservative 0; Mismatches 9;
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PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PRILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-09-09
                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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; LOCATION: (1)...(865)
; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-2087

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OTHER INFORMATION: n = A,T,C or G
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LOCATION: (1)...(865)
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TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 1695
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                                                                                            GENERAL INCRMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

PRICH APPLICATION NUMBER: US 60/198,676

PRICH APPLICATION NUMBER: US 60/193,483

PRICH FILING DATE: 2000-09-20

PRICH APPLICATION NUMBER: US 60/193,483

PRICH FILING DATE: 2000-03-29

PRICH FILING DATE: 2000-03-29

PRICH FILING DATE: 1999-11-23

PRICH FILING DATE: 1999-11-23

PRICH FILING DATE: 1999-09-28

PRICH FILING DATE: 1999-08-09

PRICH FILING DATE: 1999-08-09

PRICH FILING DATE: 1999-08-09

PRICH FILING DATE: 1999-08-09

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: PARKENDER PRICH PARKEND
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIPJUS.
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR APPLICATION NUMBER: US/10/10801/08631
PRIOR PILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-31
PRIOR PLING DATE: 2000-03-31
PRIOR APPLICATION NUMBER: 09/649,167
PRIOR PILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NO 13360
LENGTH: 1637
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Publication No. US20050196754A1
GENERAL INFORMATION:
Sequence 2087, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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LOCATION: (1)...(865)

OTHER INFORMATION: n = A,T,C or G

US-10-027-632-2087
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ORGANISM: Homo sapiens
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LOCATION: (241)..(849)
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ORGANISM: Human
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NAME/KEY: SIMILAR
LOCATION: (85)...(2142)
OTHER INFORMATION: 97% homologous to Homo sapiens putative p150,accession number
OTHER INFORMATION: U93563,Smith-Waterman Score=3485.
OTHER INFORMATION: 100% homologous to Homo sapiens endoglycan, accession number OTHER INFORMATION: AF219137, Smith-Waterman Score=1070.
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71.2%; Score 35.6; DB 24; Length 1695;
Best Local Similarity 82.0%; Pred. No. 7.6e-05;
Matches 41; Conservative 0; Mismatches 9; Indels 0;
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Userout 1349, Application US/10450763

Sequence 13349, Application US/10450763

Publication No. US20050196754A1

GENERAL INFORMATION:

APPLICATION:

FILE REPERENCE: 790C1P3/US

CURRENT FILING DATE: 2003-06-11

PRIOR APPLICATION NUMBER: US/10/450,763

PRIOR FILING DATE: 2000-03-30

PRIOR PILING DATE: 2000-03-30

PRIOR PILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

PRIOR FILING DATE: 2000-03-31

NUMBER OF SEQ ID NOS: 60736

SOFTWARE: CURLED NOS: 60736
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 790CIP3/US
CURRENT APPLICATION NUMBER: US/10/450,763
CURRENT FILING DATE: 2003-06-11
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-30
PRIOR FILING DATE: 2001-03-31
PRIOR FILING DATE: 2000-03-31
                                                                                                                                                                                                                                Query Match 71.2%; Score 35.6; DB 24; Best Local Similarity 82.0%; Pred. No. 7.6e-05; Matches 41; Conservative 0; Mismatches 9;
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                                                                                NAME/KEY: misc_feature

| LOCATION: (1) ... (1637)

| OTHER INFORMATION: n = a,t,c or g

US-10-450-763-13360
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| LOCATION: (1)...(1695)

| CTHER INFORMATION: n = a,t,c or g

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PRIOR APPLICATION NUMBER: 09/649,167
PRIOR FILING DATE: 2000-08-23
NUMBER OF SEQ ID NOS: 60736
SEQ ID NOS 60736
TAPE: Userom
ORGANISM: Homo sapiens
FATURE:
NAME/KEY: SIMILAR
LOCATION: (1514)...(1942)
OTHER INPORMATION: 100% homologous to Cloning vector pSacBII SacB, accession
OTHER INPORMATION: number U09128, Smith-Waterman Score=768.
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Search completed: October 25, 2005, 06:13:42 Job time : 106.689 secs

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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-322-730A-114
US-08-387-874-87
US-08-899-575-41
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PCT-US95-08743-41
US-08-531-132-1
US-08-120-324-15
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US-08-907-739-114
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US-10-165-857-2
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US-08-276-852-41
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                                                                                                                                                                                                                                                                                                                                                    1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB
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16, Appl
11, Appl
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18, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: CALIFORNIA
COMPUTER: USA
ZIP: 92121-4362
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft MS-DOS (Version 6.0)
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,217
FILING DATE: January 9, 1997
CLASSIFICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below:
APPLICATION NUMBER: 08/221,804
FILING DATE: APPLII 1, 1994
ATTORNY/AGENT INFORMATION:
NAME: CHISTEINE A. GATLERMACHET
REGISTRATION NUMBER: 40,627
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08778217
; Patent No. 5935833
; GENERAL INFORMATION:
APPLICANT: RECOMMENTION:
TITLE OF INVENTION: Highly-Purified Recombinant
TITLE OF INVENTION: Reverse Transcriptase
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gen-Probe Incorporated
STREET: 10210 Genetic Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35.2; DB 2;
Pred. No. 9.6e-06;
0; Mismatches 8;
US-09-702-705-639
US-09-736-47-639
US-09-614-124B-639
US-09-614-639
US-09-589-184-639
US-09-334-818A-7
US-09-334-818A-10
US-09-334-818A-10
US-09-334-818A-10
US-09-334-818A-16
US-09-334-818A-16
US-09-334-818A-19
US-09-334-818A-15
US-09-334-818A-15
                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 40,627
REFERENCE/DOCKET NUMBER: MOL2A-A01F01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (619) 410-8926
TELEFAX: (619) 410-8928
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 83.3%;
Matches 40; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: Single
; TOPOLOGY: linear
US-08-778-217-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Diego
STATE: California
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US-09-397-955C-1
                                                                                                                                                                                                             TYPE: DNA
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Matches
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GENERAL INFORMATION:
APPLICANT: RIGGS, Michael G.
APPLICANT: SORBNESN, MACTHAW
APPLICANT: SORBNESN, MACTHAW
TITLE OF INVENTION: MOLONEY MURINE LEUKEMIA VIRUS
FILE REFERENCE: GPOS9-05.CP1
CURRENT APPLICATION NUMBER: US/09/397,955C
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 08/821,948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: ATTAINS OF THE CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER:
PILING DATE: May 18, 1995
APPLICATION NUMBER: 08/43,781
FILING DATE: April 1, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Christine A. Gritzmacher
REGISTRATION NUMBER: 40,627
REFERENCE/DOCKET NUMBER: 40,627
RELEPHONE: (619) 410-8926
TELEPHONE: (619) 410-8926
TELEPHONE: (619) 410-8928
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.4%; Score 35.2; DB 2; Length 114; ilarity 83.3%; Pred. No. 9.6e-06; Conservative 0; Mismatches 8; Indels (
TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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                                                                                                       US-08-12.

Sequence 1, Application US/08821948

Patent No. 5998195

GENERAL INFORMATION:

APPLICANT: Racian et al.

TITLE OF INVENTION: Highly-Purified Recombinant

TITLE OF INVENTION: Reverse Transcriptase

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Gen-Probe Incorporated

STREET: 10210 Genetic Center Drive
                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 92121-4362
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft MS-DOS (Version 6.0)
SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/821,948
FILING DATE: March 22, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09397955C
Patent No. 6593120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
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STREET: 10210
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Oligonucleotide used to construct plasmid pUC 18N
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APPLICANT: Barbas, Carlos F
APPLICANT: Lerner. Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
CORRESPONDENCE: 170
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                     / Match 70.4%; Score 35.2; DB 4; Length 114; Local Similarity 83.3%; Pred. No. 9.6e-06; nes 40; Conservative 0; Mismatches 8; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 Traarrecerrecerrececrececerriceaerceggaaccreres 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: HIGHLY-PURIFIED RECOMBINANT REVERSE TITLE OF INVENTION: TRANSCRIPTASE NUMBER OF SEQUENCES: 18 COMPUTER READBALLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 SOFTWARE: CURENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/04092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35.2; DB 5;
Pred. No. 9.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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PRIOR FILING DATE: 1997-03-21
PRIOR APPLICATION WINBER: 08/443,781
PRIOR FILING DATE: 1995-05-18
PRIOR APPLICATION NUMBER: 08/221,804
PRIOR PLING DATE: 1994-04-01
SUMBER OF SEQ ID NOS: 21
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US95-04092-1/c
; Sequence 1, Application PC/TUS9504092
; GENERAL INFORMATION:
; APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-276-852-41/c
; Sequence 41, Application US/08276852
Patent No. 5652138
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 118 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
PCT-US95-04092-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 40; Conservative
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CLASSIFICATION:
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Patentin Release #1.0, Version #1.25
                                                                              APPLICATION NOMBER: US/09/133,011
FILING DATE: 08-UDN-1994
CLASSIERICATION 0473.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: 34,163
REGISTRATION NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                     SCRF 238.2
                                                                                                                                                                                                                                                       PCT/US 92/03091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: US 07/683,602
FILING DATE: 10-APR-1991
                                              . US/08/133,011
08-JUN-1994
1: лэг
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 70.4%;
Best Local Similarity 83.3%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ANTI-SENSE:
US-08-133-011-114
                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
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0
SSEB: Patent Counsel
T: 10666 No. 5652138th Torrey Pines Road, Suite 220, ra Mail Drop TPC8
La Jolla
CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 70.4%; Score 35.2; DB 1; Length 201; Best Local Similarity 83.3%; Pred. No. 1.1e-05; Matches 40; Conservative 0; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                 ADDRESSEE: The Scripps Research Institute, Office of
                                                                                                                                                                         COMPUTER FALSABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: ELEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/276,852
FILING DATE: 18-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
RIOR APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1993
ATORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERNEC/DOCKET NUMBER: 36,163
RELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEPAX: 619-554-6312
INFORMATION FOR SEG ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYRE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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CA
                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JS-08-133-011-114/c
                                                                                                                                                                92037
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                                                                                   STREET: NCITY: La STATE: CACOUNTRY:
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Gaps
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Sequence 114, Application US/08322730A

Patent No. 575981.

GENERAL INFORMATION:
APPLICANT: Barbas, Carlos

TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING TITLE OF INVENTION: PHAGEMIDS

NUMBER OF SEQUENCES: 125

CORRESPONDENCE ADDRESS:
ADDRESSEE: The SCTIPUS Research Institute, Office of ADDRESSEE: Patent Counsel

STREET: 10550 No. 5759817th Torrey Pines Road, Suite 220, STREET: Mail Drop TPC8

CITY: La Johla

STREET: CA.
                                                           ö
Score 35.2; DB 1; Length 201; Pred. No. 1.1e-05; 0; Mismatches 8; Indels 0
                                                                                                                                                65 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 18
                                                                                                                   3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/322,730A
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MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
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US-08-899-575-41/c
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                                                 ; ANTI-SENSE:
US-08-387-874-87
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STATE:
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Sequence 87, Application US/08387874

Sequence 87, Application US/08387874

Sequence 87, Application US/08387874

Sequence 87, Application

APPLICANT: Lerner, Richard A.

APPLICANT: Lerner, Richard A.

TITLE OF INVENTION: PHAGBAIDS COEXPRESSING A SURFACE

TITLE OF INVENTION: RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN

NUMBER OF SEQUENCES, 97

CORRESPONDENCE ADDRESS:

ADDRESSEE: The Scripps Research Institute, Office of

ADDRESSEE: Patent Counsel

STREET: 10666 No. 5770356th Torrey Pines Road, Suite 220,

STREET: Mail Drop TPC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,874

FILING DATE: 22-FEB-1995

PROOF APPLICATION DATA:

APPLICATION NUMBER: US/08/387,874

FILING DATE: 03-2FEB-1995

PROOF APPLICATION NUMBER: US/08/364

FILING DATE: 03-8EP-1993

PROOF APPLICATION NUMBER: US 07/941,369

FILING DATE: 04-8EP-1992

ATONEVAGENT INPOMMATION:

NAME: FILLING, Thomas

REGISTRATION NUMBER: 34,163

REGISTRATION NUMBER: 15ELEPAN: 619-554-2937

TELEPHONE: 619-554-2937

TELEPAN: 619-554-2937

TELEPAN: 619-554-1937

SEQUIRNE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35.2; DB 1;
Pred. No. 1.1e-05;
0; Mismatches 8;
               NAME: Bingham, Douglas A
REGISTRATION NUMBER: 32,457
REFERENCE/DOCKET NUMBER: 3C.857
TELECOMMUNICATION INFORMATION:
TELEPRONE: 619-784-237
TELEPRONE: 619-784-339
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: Gouble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 70.4%;
Best Local Similarity 83.3%;
Matches 40; Conservative
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   La Jolla
CA
                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE: NO
US-08-322-730A-114
                                                                                                                                                                                                                                                                                               TOPOLOGY: lir
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
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0
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0
                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Burton, Dennis R
APPLICANT: Burton, Dennis R
APPLICANT: Burbas, Carlos F
APPLICANT: Burbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
TITLE OF INVENTION: TO HUMAN IMMUNOBERICIENCY VIRUS
TO SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
                                                                                                            20
Score 35.2; DB 1; Length 201;
Pred. No. 1.1e-05;
0; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 70.4%; Score 35.2; DB 1; Length 201; Best Local Similarity 83.3%; Pred. No. 1.1e-05; Matches 40; Conservative 0; Mismatches 8; Indels
                                                                                                            3 TTAAGCTTATAGCGATGACTGCCCCCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                  65 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: LATENTY DATA:
APPLICATION NUMBER: US/08/899,575
FTI.ING DATE: 24-UUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCR1452P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                                    Sequence 41, Application US/08899575
Patent No. 5770440
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
       70.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
Query Match
Best Local Similarity 83.37
Matches 40; Conservative
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GENERAL INFORMATION:
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                                                                                                                                                                   Sequence 41, Application US/08899575
Fatent No. 5804440
GENERAL INFORMATION.
GENERAL INFORMATION.
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patent Counsel
STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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70.4%; Score 35.2; DB 1; Length 201;
Best Local Similarity 83.3%; Pred. No. 1.1e-05;
Matches 40; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50
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TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACC
                                                65 TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILING DATE: 24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-UUL-1994
APPLICATION NUMBER: US 08/178,302
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/954,148
FILING DATE: 30-SEP-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Fitting, Thomas REGISTRATION NUMBER: 34,163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: SC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-554-2937
TELEPHONE: 619-554-6312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 41: SEQUENCE CHARACTERISTICS: LENGTH: 201 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
                                                                                                                                                        JS-08-899-575-41/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
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; Sequence 114, Application US/08383619 ; Patent No. 5955341

US-08-383-619-114/c

RESULT 11

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 Traarrecerrecercacrececerriceaerceeaaacererere
APPLICANT: Kang, Angray
APPLICANT: Barbas, Carlos
APPLICANT: Barbas, Carlos
APPLICANT: Lerner, Richard
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESS:
ADDRESSEE: DOUGLAS A. BINGHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 114, Application US/08907739
Patent No. 6235469
GENERAL INFORMATION:
APPLICANT: Kang, Angray
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
TITLE OF INVENTION: PHAGEMIDS
NUMBER OF SEQUENCES: 161
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
STREET: 10666 No. 6235469th Torrey Pines Road, TPC-8
CITY: La Jolla
                                                                                                                                                                                                                                                                  ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,619
FILING DATE:
                                                                                                                                                         ADDRESSEE: DOUGLAS A. BINGHAM
STREET: 11300 Sorrento Valley Road, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.4%; Score 35.2; DB 2; 83.3%; Pred. No. 1.1e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: APPLICATION NUMBER: US/07/683,602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCR0371P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Bingham, Douglas A.
REGISTATION UNDMER: 32.45.
REFERENCE/DOCKET NUMBER: SCRO:
TELECOMMUNICATION INFORMATION:
TELEMONE: 615-546-1555
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                        California
: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3%
Watches 40; Conservative
                                                                                                                                                                                                          CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-907-739-114/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-383-619-114
                                                                                                                                                                                                                          STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: C. COUNTRY: ZIP: 920:
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PHAGEMIDS COEXPRESSING A SURFACE RECEPTOR AND A SURFACE HETEROLOGOUS PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 Traarrecerrecercececececres 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTLE OF INVENTION: PHAGEMIDS COEXPRESSING A SURFACE
TITLE OF INVENTION: RECEPTOR AND A SURFACE HETEROLOGOUS PR
NUMBER OF SEQUENCES: 97
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION NUMBER: PCT/US93/08364
FILING DATE: 03-SEP-1993
PRING APPLICATION NUMBER: US 07/941,369
FILING DATE: 04-SEP-1992
INFORMATION POR SEQ ID NO: 87:
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              APPLICATION NUMBER: 08/133,011
FILING DATE: 1994-09-29
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-47N-1992
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTORNAY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: SCRF 238.2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAG
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SEQUENCE DESCRIPTION: SEQ ID NO: 114:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 87, Application PC/TUS9308364 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                          TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 114:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 83.3
Matches 40; Conservative
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
PCT-US93-08364-87/c
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US-09-729-597-114/c
US-09-729-597-114/c
Sequence 114, Application US/09729597
Patent No. 6468738
GENERAL INFORMATION:
HAPPLICANT: Kang, Angray
Barbas, Carlos
Lerner, Richard A.
TITLE OF INVENTION: HETERODIMERIC RECEPTOR LIBRARIES USING
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CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10666 No. 6468738th Torrey Pines Road, TPC-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 TTAATTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG
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COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/729,597
FILING DATE: 04-Dec-2000
CLASSIFICATION: 435
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/907,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Pest Local Similarity 83.3%; Pred. No. 1.1e-05;
Matches 40; Conservative 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: 36.2
TELECOMUNICATION INFORMATION:
TELEPAR: 619-554-6317
INFORMATION FOR SEQ ID NO: 5EQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US 92/03091
FILING DATE: 10-APR-1992
ATTORNEX/AGENT INFORMATION:
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APPLICATION NUMBER: 08/133,011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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ZIP: 92037
COMPUTER READABLE FORM:
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                                                                                                                                                                                 CLASSIFICATION:
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                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                            FILING DATE:
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Query Match
70.4%; Score 35.2; DB 5; Length 201;
Best Local Similarity 83.3%; Pred. No. 1.1e-05;
Matches 40; Conservative 0; Mismatches 8; Indels (
RESULT 15
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3 TTAAGCTTATAGCGATGACTGCCCGCTTTCCAGTCGGGAAACCTGTCG 50

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Search completed: October 24, 2005, 21:57:51 Job time : 19.0038 secs

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